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(54) Title: NOVEL PESTICIDAL PROTEINS AND STRAINS		
(57) Abstract		
<p>The present invention is drawn to pesticidal strains and proteins. <i>Bacillus</i> strains which are capable of producing pesticidal proteins and auxiliary proteins during vegetative growth are provided. Also provided are the purified proteins, nucleotide sequences encoding the proteins and methods for using the strains, proteins and genes for controlling pests.</p>		

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NOVEL PESTICIDAL PROTEINS AND STRAINS

The present invention is drawn to methods and compositions for controlling plant and non-plant pests. Particularly, new pesticidal proteins are disclosed which are isolatable from the vegetative growth stage of *Bacillus*. *Bacillus* strains, proteins, and genes encoding the proteins are provided. The methods and compositions of the invention may be used in a variety of systems for controlling plant and non-plant pests.

Insect pests are a major factor in the loss of the world's commercially important agricultural crops. Broad spectrum chemical pesticides have been used extensively to control or eradicate pests of agricultural importance. There is, however, substantial interest in developing effective alternative pesticides.

Microbial pesticides have played an important role as alternatives to chemical pest control. The most extensively used microbial product is based on the bacterium *Bacillus thuringiensis* (Bt). Bt is a gram-positive spore forming *Bacillus* which produces an insecticidal crystal protein (ICP) during sporulation.

Numerous varieties of Bt are known that produce more than 25 different but related ICP's. The majority of ICP's made by Bt are toxic to larvae of certain insects in the orders *Lepidoptera*, *Diptera* and *Coleoptera*. In general, when an ICP is ingested by a susceptible insect the crystal is solubilized and transformed into a toxic moiety by the insect gut proteases. None of the ICP's active against coleopteran larvae such as Colorado potato beetle (*Leptinotarsa decemlineata*) or Yellow mealworm (*Tenebrio molitor*) have demonstrated significant effects on members of the genus *Diabrotica* particularly *Diabrotica virgifera virgifera*, the western corn rootworm (WCRW) or *Diabrotica longicornis barberi*, the northern corn rootworm.

Bacillus cereus (Bc) is closely related to Bt. A major distinguishing characteristic is the absence of a parasporal crystal in Bc. Bc is a widely distributed bacterium that is commonly found in soil and has been isolated from a variety of foods and drugs. The organism has been implicated in the spoilage of food.

Although Bt has been very useful in controlling insect pests, there is a need to expand the number of potential biological control agents.

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Within the present invention compositions and methods for controlling plant pests are provided. In particular, novel pesticidal proteins are provided which are produced during vegetative growth of *Bacillus* strains. The proteins are useful as pesticidal agents.

More specifically, the present invention relates to a substantially purified *Bacillus* strain which produces a pesticidal protein during vegetative growth wherein said *Bacillus* is not *B. sphaericus* SSII-1. Preferred are a *Bacillus cereus* strain having Accession No. NRRL B-21058 and *Bacillus thuringiensis* strain having Accession No. NRRL B-21060. Also preferred is a *Bacillus* strain selected from Accession Numbers NRRL B-21224, NRRL B-21225, NRRL B-21226, NRRL B-21227, NRRL B-21228, NRRL B-21229, NRRL B-21230, and NRRL B-21439.

The invention further relates to an insect-specific protein isolatable during the vegetative growth phase of *Bacillus* spp, but preferably of a *Bacillus thuringiensis* and *B. cereus* strain, and components thereof, wherein said protein is not the mosquitocidal toxin from *B. sphaericus* SSII-1. The insect-specific protein of the invention is preferably toxic to Coleoptera or Lepidoptera insects and has a molecular weight of about 30 kDa or greater, preferably of about 60 to about 100 kDa, and more preferably of about 80 kDa.

More particularly, the insect-specific protein of the invention has a spectrum of insecticidal activity that includes an activity against *Agrotis* and/or *Spodoptera* species, but preferably a black cutworm [*Agrotis ipsilon* ; BCW] and/or fall armyworm [*Spodoptera frugiperda*] and/or beet armyworm [*Spodoptera exigua*] and/or tobacco budworm and/or corn earworm [*Helicoverpa zea*] activity.

The insect-specific protein of the invention can preferably be isolated, for example, from *Bacillus cereus* having Accession No. NRRL B-21058, or from *Bacillus thuringiensis* having Accession No. NRRL B-21060.

The insect-specific protein of the invention can also preferably be isolated from a *Bacillus* spp strain selected from Accession Numbers NRRL B-21224, NRRL B-21225, NRRL B-21226, NRRL B-21227, NRRL B-21228, NRRL B-21229, NRRL B-21230, and NRRL B-21439.

The present invention especially encompasses an insect-specific protein that has the amino acid sequence selected from the group consisting of SEQ ID NO:5 and

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SEQ ID NO:7, including any proteins that are structurally and/or functionally homologous thereto.

Further preferred is an insect-specific protein, wherein said protein has the sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:29, SEQ ID NO:32 and SEQ ID NO:2, including any proteins that are structurally and/or functionally homologous thereto.

Especially preferred is an insect-specific protein, wherein said protein has the sequence selected from the group consisting of SEQ ID NO:29 and SEQ ID NO:32, including any proteins that are structurally and/or functionally homologous thereto.

A further preferred embodiment of the invention comprises an insect-specific protein of the invention, wherein the sequences representing the secretion signal have been removed or inactivated.

The present invention further encompasses auxiliary proteins which enhance the insect-specific activity of an insect-specific protein. The said auxiliary proteins preferably have a molecular weight of about 50 kDa and can be isolated, for example, from the vegetative growth phase of a *Bacillus cereus* strain, but especially of *Bacillus cereus* strain AB78.

A preferred embodiment of the invention relates to an auxiliary protein, wherein the sequences representing the secretion signal have been removed or inactivated.

The present invention further relates to multimeric pesticidal proteins, which comprise more than one polypeptide chain and wherein at least one of the said polypeptide chains represents an insect-specific protein of the invention and at least one of the said polypeptide chains represents an auxiliary protein of the invention, which activates or enhances the pesticidal activity of the said insect-specific protein.

The multimeric pesticidal proteins according to the invention preferably have a molecular weight of about 50 kDa to about 200 kDa.

The invention especially encompasses a multimeric pesticidal protein, which comprises an insect-specific protein of the invention and an auxiliary protein according to the invention, which activates or enhances the pesticidal activity of the said insect-specific protein.

The present invention further relates to fusion proteins comprising several protein domains including at least an insect-specific protein of the invention and/or an auxiliary protein according to the invention produced by in frame genetic fusions,

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which, when translated by ribosomes, produce a fusion protein with at least the combined attributes of the insect-specific protein of the invention and/or an auxiliary protein according to the invention and, optionally, of the other components used in the fusion.

A specific embodiment of the invention relates to a fusion protein comprising a ribonuclease S-protein, an insect-specific protein of the invention and an auxiliary protein according to the invention.

A further specific embodiment of the invention relates to a fusion protein comprising an insect-specific protein according to the invention and an auxiliary protein according to the invention having either the insect-specific protein or the auxiliary protein at the N-terminal end of the said fusion protein.

Preferred is a fusion protein, which comprises an insect-specific protein as given in SEQ ID NO:5 and an auxiliary protein as given in SEQ ID NO: 2 resulting in the protein given in SEQ ID NO: 23, including any proteins that are structurally and/or functionally homologous thereto.

Also preferred is a fusion protein, which comprises an insect-specific protein as given in SEQ ID NO:35 and an auxiliary protein as given in SEQ ID NO: 27 resulting in the protein given in SEQ ID NO: 50, including any proteins that are structurally and/or functionally homologous thereto.

The invention further relates to a fusion protein comprising an insect-specific protein of the invention and/or an auxiliary protein according to the invention fused to a signal sequence, preferably a secretion signal sequence or a targeting sequence that directs the transgene product to a specific organelle or cell compartment, which signal sequence is of heterologous origin with respect to the recipient protein.

Especially preferred within this invention is a fusion protein wherein the said protein has a sequence as given in SEQ ID NO: 43, or in SEQ ID NO: 46, including any proteins that are structurally and/or functionally homologous thereto.

As used in the present application, substantial sequence homology means close structural relationship between sequences of amino acids. For example, substantially homologous proteins may be 40% homologous, preferably 50% and most preferably 60% or 80% homologous, or more. Homology also includes a relationship wherein one or several subsequences of amino acids are missing, or subsequences with additional amino acids are interdispersed.

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A further aspect of the invention relates to a DNA molecule comprising a nucleotide sequence which encodes an insect-specific protein isolatable during the vegetative growth phase of *Bacillus* spp. and components thereof, wherein said protein is not the mosquitocidal toxin from *B. sphaericus* SSII-1. In particular, the present invention relates to a DNA molecule comprising a nucleotide sequence which encodes an insect-specific protein wherein the spectrum of insecticidal activity includes an activity against *Agrotis* and/or *Spodoptera* species, but preferably a black cutworm [*Agrotis ipsilon* ; BCW] and/or fall armyworm [*Spodoptera frugiperda*] and/or beet armyworm [*Spodoptera exigua*] and/or tobacco budworm and/or corn earworm [*Helicoverpa zea*] activity.

Preferred is a DNA molecule, wherein the said molecule comprises a nucleotide sequence as given in SEQ ID NO: 4, or SEQ ID NO: 6, including any DNA molecules that are structurally and/or functionally homologous thereto.

Also preferred is a DNA molecule, wherein the said molecule comprises a nucleotide sequence as given SEQ ID NO:19, SEQ ID NO:28, SEQ ID NO:31, or SEQ ID NO:1, including any DNA molecules that are structurally and/or functionally homologous thereto.

The invention further relates to a DNA molecule comprising a nucleotide sequence which encodes an auxiliary protein according to the invention which enhances the insect-specific activity of an insect-specific protein.

Preferred is a DNA molecule, wherein the said molecule comprises a nucleotide sequence as given SEQ ID NO:19, including any DNA molecules that are structurally and/or functionally homologous thereto.

A further embodiment of the invention relates to a DNA molecule comprising a nucleotide sequence which encodes an insect-specific protein isolatable during the vegetative growth phase of *Bacillus* spp. and components thereof, wherein said protein is not the mosquitocidal toxin from *B. sphaericus* SSII-1, which nucleotide sequence has been optimized for expression in a microorganism or a plant.

Preferred is a DNA molecule, wherein the said molecule comprises a nucleotide sequence as given in SEQ ID NO:17 or SEQ ID NO:18, including any DNA molecules that are structurally and/or functionally homologous thereto.

Also preferred is a DNA molecule, wherein the said molecule comprises a nucleotide sequence as given in SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:27, or

SEQ ID NO:30, including any DNA molecules that are structurally and/or functionally homologous thereto.

The invention further relates to a DNA molecule which comprises a nucleotide sequence encoding a multimeric pesticidal protein, which comprises more than one polypeptide chains and wherein at least one of the said polypeptide chains represents an insect-specific protein of the invention and at least one of the said polypeptide chains represents an auxiliary protein according to the invention, which activates or enhances the pesticidal activity of the said insect-specific protein.

Preferred is a DNA molecule comprising a nucleotide sequence encoding an insect-specific protein of the invention and an auxiliary protein according to the invention, which activates or enhances the pesticidal activity of the said insect-specific protein.

Especially preferred is a DNA molecule, wherein said molecule comprises a nucleotide sequence as given in SEQ ID NO:1 or SEQ ID NO:19, including any nucleotide sequences that are structurally and/or functionally homologous thereto. A further embodiment of the invention relates to a DNA molecule which comprises a nucleotide sequence encoding a fusion protein comprising several protein domains including at least an insect-specific protein of the invention and/or an auxiliary protein according to the invention produced by in frame genetic fusions, which, when translated by ribosomes, produce a fusion protein with at least the combined attributes of the insect-specific protein of the invention and/or an auxiliary protein according to the invention and, optionally, of the other components used in the fusion.

Preferred within the invention is a DNA molecule which comprises a nucleotide sequence encoding a fusion protein comprising an insect-specific protein according to the invention and an auxiliary protein according to the invention having either the insect-specific protein or the auxiliary protein at the N-terminal end of the said fusion protein. Especially preferred is a DNA molecule, wherein the said molecule comprises a nucleotide sequence as given in SEQ ID NO:22, including any DNA molecules that are structurally and/or functionally homologous thereto.

The invention further relates to a DNA molecule which comprises a nucleotide sequence encoding a fusion protein comprising an insect-specific protein of the invention and/or an auxiliary protein of the invention fused to a signal sequence, preferably a secretion signal sequence or a targeting sequence that directs the

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transgene product to a specific organelle or cell compartment, which signal sequence is of herterologous origin with respect to the recipient DNA.

The present invention further encompasses a DNA molecule comprising a nucleotide sequence encoding a fusion protein or a mulitmeric protein according to the invention that has been optimized for expression in a microorganism or plant.

Preferred is an optimized DNA molecule, wherein the said molecule comprises a nucleotide sequence as given in SEQ ID NO:42, SEQ ID NO:45, or SEQ ID NO:49, including any DNA molecules that are structurally and/or functionally homologous thereto.

The invention further relates to an optimized DNA molecule, wherein the sequences encoding the secretion signal have been removed from its 5' end, but especially to an optimized DNA molecule, wherein the said molecule comprises a nucleotide sequence as given in SEQ ID NO: 35 or SEQ ID NO:39, including any DNA molecules that are structurally and/or functionally homologous thereto.

As used in the present application, substantial sequence homology means close structural relationship between sequences of nucleotides. For example, substantially homologous DNA molecules may be 60% homologous, preferably 80% and most preferably 90% or 95% homologous, or more. Homology also includes a relationship wherein one or several subsequences of nucleotides or amino acids are missing, or subsequences with additional nucleotides or amino acids are interdispersed.

Also comprised by the present invention are DNA molecules which hybridizes to a DNA molecule according to the invention as defined hereinbefore, but preferably to an oligonucleotide probe obtainable from said DNA molecule comprising a contiguous portion of the coding sequence for the said insect-specific protein at least 10 nucleotides in length, under moderately stringent conditions and which molecules have insect-specific activity and also the insect-specific proteins being encoded by the said DNA molecules.

Preferred are DNA molecules, wherein hybridization occurs at 65°C in a buffer comprising 7% SDS and 0.5 M sodium phosphate.

Especially preferred is a DNA molecule comprising a nucleotide sequence which encodes an insect-specific protein according to the invention obtainable by a process comprising

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- (a) obtaining a DNA molecule comprising a nucleotide sequence encoding an insect-specific protein; and
- (b) hybridizing said DNA molecule with an oligonucleotide probe according to claim 107 obtained from a DNA molecule comprising a nucleotide sequence as given in SEQ ID NO: 28, SEQ ID NO: 30, or SEQ ID NO: 31; and
- (c) isolating said hybridized DNA.

The invention further relates to an insect-specific protein, wherein the said protein is encoded by a DNA molecule according to the invention.

Also encompassed by the invention is an expression cassette comprising a DNA molecule according to the invention operably linked to expression sequences including the transcriptional and translational regulatory signals necessary for expression of the associated DNA constructs in a host organism, preferably a microorganism or a plant, and optionally further regulatory sequences.

The invention further relates to a vector molecule comprising an expression cassette according to the invention.

The expression cassette and/or the vector molecule according to the invention are preferably part of the plant genome.

A further embodiment of the invention relates to a host organism, preferably a host organism selected from the group consisting of plant and insect cells, bacteria, yeast, baculoviruses, protozoa, nematodes and algae, comprising a DNA molecule according to the invention, an expression cassette comprising the said DNA molecule or a vector molecule comprising the said expression cassette, preferably stably incorporated into the genome of the host organism.

The invention further relates to a transgenic plant, but preferably a maize plant, including parts as well as progeny and seed thereof comprising a DNA molecule according to the invention, an expression cassette comprising the said DNA molecule or a vector molecule comprising the said expression cassette, preferably stably incorporated into the plant genome.

Preferred is a transgenic plant including parts as well as progeny and seed thereof which has been stably transformed with a DNA molecule according to the invention, an expression cassette comprising the said DNA molecule or a vector molecule comprising the said expression cassette.

Also preferred is a transgenic plant including parts as well as progeny and seed thereof which expresses an insect-specific protein according to the invention.

The invention further relates to a transgenic plant, preferably a maize plant, according to the invention as defined hereinbefore, which further expresses a second distinct insect control principle, but preferably a *Bt* δ -endotoxin. The said plant is preferably a hybrid plant.

Parts of transgenic plants are to be understood within the scope of the invention to comprise, for example, plant cells, protoplasts, tissues, callus, embryos as well as flowers, stems, fruits, leaves, roots originating in transgenic plants or their progeny previously transformed with a DNA molecule according to the invention and therefore consisting at least in part of transgenic cells, are also an object of the present invention.

The invention further relates to plant propagating material of a plant according to the invention, which is treated with a seed protectant coating.

The invention further encompasses a microorganism transformed with a DNA molecule according to the invention, an expression cassette comprising the said DNA molecule or a vector molecule comprising the said expression cassette, wherein the said microorganism is preferably a microorganism that multiply on plants and more preferably a root colonizing bacterium.

A further embodiment of the invention relates to an encapsulated insect-specific protein which comprises a microorganism comprising an insect specific protein according to the invention.

The invention also relates to an entomocidal composition comprising a host organism of the invention, but preferably a purified *Bacillus* strain, in an insecticidally-effective amount together with a suitable carrier.

Further comprised by the invention is an entomocidal composition comprising an isolated protein molecule according to the invention, alone or in combination with a host organism of the invention and/or an encapsulated insect-specific protein according to the invention, in an insecticidally-effective amount, together with a suitable carrier.

A further embodiment of the invention relates to a method of obtaining a purified insect-specific protein according to the invention, said method comprising applying a

solution comprising said insect-specific protein to a NAD column and eluting bound protein.

Also comprised is a method for identifying insect activity of an insect-specific protein according to the invention, said method comprising:

- growing a *Bacillus* strain in a culture;
- obtaining supernatant from said culture;
- allowing insect larvae to feed on diet with said supernatant; and,
- determining mortality.

Another aspect of the invention relates to a method for isolating an insect-specific protein according to the invention, said method comprising:

- growing a *Bacillus* strain in a culture;
- obtaining supernatant from said culture; and,
- isolating said insect-specific protein from said supernatant.

The invention also encompasses a method for isolating a DNA molecule comprising a nucleotide sequence encoding an insect-specific protein exhibiting the insecticidal activity of the proteins according to the invention, said method comprising:

- obtaining a DNA molecule comprising a nucleotide sequence encoding an insect-specific protein; and
- hybridizing said DNA molecule with DNA obtained from a *Bacillus* species;
- and
- isolating said hybridized DNA.

The invention further relates to a method of increasing insect target range by using an insect specific protein according to the invention in combination with at least one second insecticidal protein that is different from the insect specific protein according to the invention, but preferably with an insecticidal protein selected from the group consisting of *Bt* δ -endotoxins, protease inhibitors, lectins, α -amylases and peroxidases.

Preferred is a method for increasing insect target range within a plant by expressing within the said plant a insect specific protein according to the invention in combination with at least one second insecticidal protein that is different from the insect specific protein according to the invention, but preferably with an insecticidal protein selected from the group consisting of *Bt* δ -endotoxins, protease inhibitors, lectins, α -amylases and peroxidases.

Also comprised is a method of protecting plants against damage caused by an insect pest, but preferably by *Spodoptera* and/or *Agrotis* species, and more preferably by an insect pest selected from the group consisting of black cutworm [*Agrotis ipsilon* ; BCW], fall armyworm [*Spodoptera frugiperda*], beet armyworm [*Spodoptera exigua*], tobacco budworm and corn earworm [*Helicoverpa zea*] comprising applying to the plant or the growing area of the said plant an entomocidal composition or a toxin protein according to the invention.

The invention further relates to method of protecting plants against damage caused by an insect pest, but preferably by *Spodoptera* and/or *Agrotis* species, and more preferably by an insect pest selected from the group consisting of black cutworm [*Agrotis ipsilon* ; BCW], fall armyworm [*Spodoptera frugiperda*], beet armyworm [*Spodoptera exigua*], tobacco budworm and corn earworm [*Helicoverpa zea*] comprising planting a transgenic plant expressing a insect-specific protein according to the invention within an area where the said insect pest may occur.

The invention also encompasses a method of producing a host organism which comprises stably integrated into its genome a DNA molecule according to the invention and preferably expresses an insect-specific protein according to the invention comprising transforming the said host organism with a DNA molecule according to the invention, an expression cassette comprising the said DNA molecule or a vector molecule comprising the said expression cassette.

A further embodiment of the invention relates to a method of producing a transgenic plant or plant cell which comprises stably integrated into the plant genome a DNA molecule according to the invention and preferably expresses an insect-specific protein according to the invention comprising transforming the said plant and plant cell, respectively, with a DNA molecule according to the invention, an expression cassette comprising the said DNA molecule or a vector molecule comprising the said expression cassette.

The invention also relates to a method of producing an entomocidal composition comprising mixing an isolated *Bacillus* strain and/or a host organism and/or an isolated protein molecule, and/or an encapsulated protein according to the invention in an insecticidally-effective amount with a suitable carrier.

The invention also encompasses a method of producing transgenic progeny of a transgenic parent plant comprising stably incorporated into the plant genome a DNA

molecule comprising a nucleotide sequence encoding an insect-specific protein according to the invention comprising transforming the said parent plant with a DNA molecule according to the invention, an expression cassette comprising the said DNA molecule or a vector molecule comprising the said expression cassette and transferring the pesticidal trait to the progeny of the said transgenic parent plant involving known plant breeding techniques.

Also encompassed by the invention is oligonucleotide probe capable of specifically hybridizing to a nucleotide sequence encoding a insect-specific protein isolatable during the vegetative growth phase of *Bacillus* spp. and components thereof, wherein said protein is not the mosquitocidal toxin from *B. sphaericus* SSII-1, wherein said probe comprises a contiguous portion of the coding sequence for the said insect-specific protein at least 10 nucleotides in-length and the use of the said oligonucleotide probe for screening of any *Bacillus* strain or other organisms to determine whether the insect-specific protein is naturally present or whether a particular transformed organism includes the said gene

The present invention recognizes that pesticidal proteins are produced during vegetative growth of *Bacillus* strains. Having recognized that such a class exists, the present invention embraces all vegetative insecticidal proteins, hereinafter referred to as VIPs, except for the mosquitocidal toxin from *B. sphaericus*.

The present VIPs are not abundant after sporulation and are particularly expressed during log phase growth before stationary phase. For the purpose of the present invention vegetative growth is defined as that period of time before the onset of sporulation. Genes encoding such VIPs can be isolated, cloned and transformed into various delivery vehicles for use in pest management programs.

For purposes of the present invention, pests include but are not limited to insects, fungi, bacteria, nematodes, mites, ticks, protozoan pathogens, animal-parasitic liver flukes, and the like. Insect pests include insects selected from the orders Coleoptera, Diptera, Hymenoptera, Lepidoptera, Mallophaga, Homoptera, Hemiptera, Orthoptera, Thysanoptera, Dermaptera, Isoptera, Anoplura, Siphonaptera, Trichoptera, etc., particularly Coleoptera and Lepidoptera.

Tables 1 - 10 gives a list of pests associated with major crop plants and pests of human and veterinary importance. Such pests are included within the scope of the present invention.

TABLE 1

Lepidoptera (Butterflies and Moth)

Maize

Ostrinia nubilalis, European corn borer
Agrotis ipsilon, black cutworm
Helicoverpa zea, corn earworm
Spodoptera frugiperda, fall armyworm
Diatraea grandiosella, southwestern corn borer
Elasmopalpus lignosellus, lesser cornstalk borer
Diatraea saccharalis, sugarcane borer

Sorghum

Chilo partellus, sorghum borer
Spodoptera frugiperda, fall armyworm
Helicoverpa zea, corn earworm
Elasmopalpus lignosellus, lesser cornstalk borer
Feltia subterranea, granulate cutworm

Wheat

Pseudaletia unipunctata, army worm
Spodoptera frugiperda, fall armyworm
Elasmopalpus lignosellus, lesser cornstalk borer
Agrotis orthogonia, pale western cutworm
Elasmopalpus lignosellus, lesser cornstalk borer

Sunflower

Suleima helianthana, sunflower bud moth
Homoeosoma electellum, sunflower moth

Cotton

Heliothis virescens, cotton boll worm
Helicoverpa zea, cotton bollworm
Spodoptera exigua, beet armyworm
Pectinophora gossypiella, pink bollworm

Rice

Diatraea saccharalis, sugarcane borer
Spodoptera frugiperda, fall armyworm
Helicoverpa zea, corn earworm

Soybean

Pseudoplusia includens, soybean looper
Anticarsia gemmatilis, velvetbean caterpillar
Plathypena scabra, green cloverworm
Ostrinia nubilalis, European corn borer
Agrotis ipsilon, black cutworm
Spodoptera exigua, beet armyworm
Heliothis virescens, cotton boll worm
Helicoverpa zea, cotton bollworm

Barley

Ostrinia nubilalis, European corn borer
Agrotis ipsilon, black cutworm

TABLE 2

Coleoptera (Beetles)

Maize

Diabrotica virgifera virgifera, western corn rootworm
Diabrotica longicornis barberi, northern corn rootworm
Diabrotica undecimpunctata howardi, southern corn rootworm
Melanotus spp., wireworms
Cyclocephala borealis, northern masked chafer (white grub)
Cyclocephala immaculata, southern masked chafer (white grub)
Popillia japonica, Japanese beetle
Chaetocnema pulicaria, corn flea beetle
Sphenophorus maidis, maize billbug

Sorghum

Phyllophaga crinita, white grub
Eleodes, *Conoderus*, and *Aeolus* spp., wireworms
Oulema melanopus, cereal leaf beetle
Chaetocnema pulicaria, corn flea beetle
Sphenophorus maidis, maize billbug

Wheat

Oulema melanopus, cereal leaf beetle
Hypera punctata, clover leaf weevil
Diabrotica undecimpunctata howardi, southern corn rootworm

Sunflower

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Zygogramma exclamationis, sunflower beetle
Bothyrus gibbosus, carrot beetle

Cotton

Anthonomus grandis, boll weevil

Rice

Colaspis brunnea, grape colaspis
Lissorhoptrus oryzophilus, rice water weevil
Sitophilus oryzae, rice weevil

Soybean

Epilachna varivestis, Mexican bean beetle

TABLE 3

Homoptera (Whiteflies, Aphids etc..)

Maize

Rhopalosiphum maidis, corn leaf aphid
Anuraphis maidiradicis, corn root aphid

Sorghum

Rhopalosiphum maidis, corn leaf aphid
Sipha flava, yellow sugarcane aphid

Wheat

Russian wheat aphid
Schizaphis graminum, greenbug
Macrosiphum avenae, English grain aphid

Cotton

Aphis gossypii, cotton aphid
Pseudatomoscelis seriatus, cotton fleahopper
Trialeurodes abutilonea, bandedwinged whitefly

Rice

Nephotettix nigropictus, rice leafhopper

Soybean

Myzus persicae, green peach aphid
Empoasca fabae, potato leafhopper

Barley

Schizaphis graminum, greenbug

Oil Seed Rape

Brevicoryne brassicae, cabbage aphid

TABLE 4

Hemiptera (Bugs)

Maize

Blissus leucopterus leucopterus, chinch bug

Sorghum

Blissus leucopterus leucopterus, chinch bug

Cotton

Lygus lineolaris, tarnished plant bug

Rice

Blissus leucopterus leucopterus, chinch bug
Acrosternum hilare, green stink bug

Soybean

Acrosternum hilare, green stink bug

Barley

Blissus leucopterus leucopterus, chinch bug
Acrosternum hilare, green stink bug
Euschistus servus, brown stink bug

TABLE 5

Orthoptera (Grasshoppers, Crickets, and Cockroaches)

Maize

Melanoplus femurrubrum, redlegged grasshopper
Melanoplus sanguinipes, migratory grasshopper

Wheat

Melanoplus femurrubrum, redlegged grasshopper
Melanoplus differentialis, differential grasshopper
Melanoplus sanguinipes, migratory grasshopper

Cotton

Melanoplus femurrubrum, redlegged grasshopper
Melanoplus differentialis, differential grasshopper

Soybean

Melanoplus femurrubrum, redlegged grasshopper
Melanoplus differentialis, differential grasshopper

Structural/Household

Periplaneta americana, American cockroach
Blattella germanica, German cockroach
Blatta orientalis, oriental cockroach

TABLE 6

Diptera (Flies and Mosquitoes)

Maize

Hylemya platura, seedcorn maggot
Agromyza parvicornis, corn blotch leafminer

Sorghum

Contarinia sorghicola, sorghum midge

Wheat

Mayetiola destructor, Hessian fly
Sitodiplosis mosellana, wheat midge
Meromyza americana, wheat stem maggot
Hylemya coarctata, wheat bulb fly

Sunflower

Neolasioptera murtfeldtiana, sunflower seed midge

Soybean

Hylemya platura, seedcorn maggot

Barley

Hylemya platura, seedcorn maggot
Mayetiola destructor, Hessian fly

Insects attacking humans and animals and disease carriers

Aedes aegypti, yellowfever mosquito
Aedes albopictus, forest day mosquito
Phlebotomus papatasi, sand fly
Musca domestica, house fly
Tabanus atratus, black horse fly
Cochliomyia hominivorax, screwworm fly

TABLE 7

Thysanoptera (Thrips)

Maize

Anaphothrips obscurus, grass thrips

Wheat

Frankliniella fusca, tobacco thrips

Cotton

Thrips tabaci, onion thrips
Frankliniella fusca, tobacco thrips

Soybean

Sericothrips variabilis, soybean thrips
Thrips tabaci, onion thrips

TABLE 8

Hymenoptera (Sawflies, Ants, Wasps, etc.)

Maize

Solenopsis milesta, thief ant

Wheat

Cephus cinctus, wheat stem sawfly

TABLE 9

Other Orders and Representative Species*Dermaptera* (Earwigs)

Forficula auricularia, European earwig

Isoptera (Termites)

Reticulitermes flavipes, eastern subterranean termite

Mallophaga (Chewing Lice)

Cuclotogaster heterographa, chicken head louse
Bovicola bovis, cattle biting louse

Anoplura (Sucking Lice)

Pediculus humanus, head and body louse

Siphonaptera (Fleas)

Ctenocephalides felis, cat flea

TABLE 10

Acari (Mites and Ticks)

Maize

Tetranychus urticae, twospotted spider mite

Sorghum

Tetranychus cinnabarinus, carmine spider mite*Tetranychus urticae*, twospotted spider mite

Wheat

Aceria tulipae, wheat curl mite

Cotton

Tetranychus cinnabarinus, carmine spider mite*Tetranychus urticae*, twospotted spider mite

Soybean

Tetranychus turkestanii, strawberry spider mite*Tetranychus urticae*, twospotted spider mite

Barley

Petrobia latens, brown wheat miteImportant human and animal *Acari**Demacentor variabilis*, American dog tick*Argas persicus*, fowl tick*Dermatophagoides farinae*, American house dust mite*Dermatophagoides pteronyssinus*, European house dust mite

Now that it has been recognized that pesticidal proteins can be isolated from the vegetative growth phase of *Bacillus*, other strains can be isolated by standard techniques and tested for activity against particular plant and non-plant pests. Generally *Bacillus* strains can be isolated from any environmental sample, including soil, plant, insect, grain elevator dust, and other sample material, etc., by methods

known in the art. See, for example, Travers *et al.* (1987) Appl. Environ. Microbiol. 53:1263-1266; Saleh *et al.* (1969) Can J. Microbiol. 15:1101-1104; DeLucca *et al.* (1981) Can. J. Microbiol. 27:865-870; and Norris, *et al.* (1981) "The genera *Bacillus* and *Sporolactobacillus*," In Starr *et al.* (eds.), The Prokaryotes: A Handbook on Habitats, Isolation, and Identification of Bacteria, Vol. II, Springer-Verlag Berlin Heidelberg. After isolation, strains can be tested for pesticidal activity during vegetative growth. In this manner, new pesticidal proteins and strains can be identified.

Such *Bacillus* microorganisms which find use in the invention include *Bacillus cereus* and *Bacillus thuringiensis*, as well as those *Bacillus* species listed in Table 11.

TABLE 11

List of *Bacillus* species

Morphological Group 1

B. megaterium
*B. cereus**
B. cereus var. *mycoides*
*B. thuringiensis**
B. licheniformis
*B. subtilis**
B. pumilus
*B. firmus**
B. coagulans

Morphological Group 2

B. polymyxa
B. macerans
B. circulans
B. stearothermophilus
*B. alvei**
*B. laterosporus**
B. brevis
B. pulvifaciens
*B. popilliae**
*B. lentimorbus**
*B. larvae**

Morphological Group 3

*B. sphaericus**
B. pasteurii

Unassigned Strains

Subgroup A

*B. apiarus**
B. filicolonicus
B. thiaminolyticus
B. alcalophilus

Subgroup B

B. cirroflagellosus
B. chitinosporus
B. lentus

Subgroup C

B. badius
B. aneurinolyticus
B. macroides
B. freundenreichii

Subgroup D

B. pantothenicus
B. epiphytus

Subgroup E1

B. aminovorans
B. globisporus
B. insolitus
B. psychrophilus

Subgroup E2

B. psychrosaccharolyticus
B. macquariensis

*=Those *Bacillus* strains that have been previously found associated with insects

Grouping according to Parry, J.M. *et al.* (1983) Color Atlas of *Bacillus* species, Wolfe Medical Publications, London.

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In accordance with the present invention, the pesticidal proteins produced during vegetative growth can be isolated from *Bacillus*. In one embodiment, insecticidal proteins produced during vegetative growth, can be isolated. Methods for protein isolation are known in the art. Generally, proteins can be purified by conventional chromatography, including gel-filtration, ion-exchange, and immunoaffinity chromatography, by high-performance liquid chromatography, such as reversed-phase high-performance liquid chromatography, ion-exchange high-performance liquid chromatography, size-exclusion high-performance liquid chromatography, high-performance chromatofocusing and hydrophobic interaction chromatography, etc., by electrophoretic separation, such as one-dimensional gel electrophoresis, two-dimensional gel electrophoresis, etc. Such methods are known in the art. See for example Current Protocols in Molecular Biology, Vols. 1 and 2, Ausubel *et al.* (eds.), John Wiley & Sons, NY (1988). Additionally, antibodies can be prepared against substantially pure preparations of the protein. See, for example, Radka *et al.* (1983) J. Immunol. 128:2804; and Radka *et al.* (1984) Immunogenetics 19:63. Any combination of methods may be utilized to purify protein having pesticidal properties. As the protocol is being formulated, pesticidal activity is determined after each purification step.

Such purification steps will result in a substantially purified protein fraction. By "substantially purified" or "substantially pure" is intended protein which is substantially free of any compound normally associated with the protein in its natural state. "Substantially pure" preparations of protein can be assessed by the absence of other detectable protein bands following SDS-PAGE as determined visually or by densitometry scanning. Alternatively, the absence of other amino-terminal sequences or N-terminal residues in a purified preparation can indicate the level of purity. Purity can be verified by rechromatography of "pure" preparations showing the absence of other peaks by ion exchange, reverse phase or capillary electrophoresis. The terms "substantially pure" or "substantially purified" are not meant to exclude artificial or synthetic mixtures of the proteins with other compounds. The terms are also not meant to exclude the presence of minor impurities which do not interfere with the biological activity of the protein, and which may be present, for example, due to incomplete purification.

Once purified protein is isolated, the protein, or the polypeptides of which it is comprised, can be characterized and sequenced by standard methods known in the art. For example, the purified protein, or the polypeptides of which it is comprised, may be fragmented as with cyanogen bromide, or with proteases such as papain, chymotrypsin, trypsin, lysyl-C endopeptidase, etc. (Oike *et al.* (1982) J. Biol. Chem. 257:9751-9758; Liu *et al.* (1983) Int. J. Pept. Protein Res. 21:209-215). The resulting peptides are separated, preferably by HPLC, or by resolution of gels and electroblotting onto PVDF membranes, and subjected to amino acid sequencing. To accomplish this task, the peptides are preferably analyzed by automated sequencers. It is recognized that N-terminal, C-terminal, or internal amino acid sequences can be determined. From the amino acid sequence of the purified protein, a nucleotide sequence can be synthesized which can be used as a probe to aid in the isolation of the gene encoding the pesticidal protein.

It is recognized that the pesticidal proteins may be oligomeric and will vary in molecular weight, number of protomers, component peptides, activity against particular pests, and in other characteristics. However, by the methods set forth herein, proteins active against a variety of pests may be isolated and characterized.

Once the purified protein has been isolated and characterized it is recognized that it may be altered in various ways including amino acid substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of the pesticidal proteins can be prepared by mutations in the DNA. Such variants will possess the desired pesticidal activity. Obviously, the mutations that will be made in the DNA encoding the variant must not place the sequence out of reading frame and preferably will not create complementary regions that could produce secondary mRNA structure. See, EP Patent Application Publication No. 75,444.

In this manner, the present invention encompasses the pesticidal proteins as well as components and fragments thereof. That is, it is recognized that component protomers, polypeptides or fragments of the proteins may be produced which retain pesticidal activity. These fragments include truncated sequences, as well as N-terminal, C-terminal, internal and internally deleted amino acid sequences of the proteins.

Most deletions, insertions, and substitutions of the protein sequence are not expected to produce radical changes in the characteristics of the pesticidal protein. However, when it is difficult to predict the exact effect of the substitution, deletion, or insertion in advance of doing so, one skilled in the art will appreciate that the effect will be evaluated by routine screening assays.

The proteins or other component polypeptides described herein may be used alone or in combination. That is, several proteins may be used to control different insect pests.

Some proteins are single polypeptide chains while many proteins consist of more than one polypeptide chain, i.e., they are oligomeric. Additionally, some VIPs are pesticidally active as oligomers. In these instances, additional protomers are utilized to enhance the pesticidal activity or to activate pesticidal proteins. Those protomers which enhance or activate are referred to as auxiliary proteins. Auxiliary proteins activate or enhance a pesticidal protein by interacting with the pesticidal protein to form an oligomeric protein having increased pesticidal activity compared to that observed in the absence of the auxiliary protein.

Auxiliary proteins activate or increase the activity of pesticidal proteins such as the VIP1 protein from AB78. Such auxiliary proteins are exemplified by, but not limited to, the VIP2 protein from AB78. As demonstrated in the Experimental section of the application, auxiliary proteins can activate a number of pesticidal proteins. Thus, in one embodiment of the invention, a plant, Parent 1, can be transformed with an auxiliary protein. This Parent 1 can be crossed with a number of Parent 2 plants transformed with one or more pesticidal proteins whose pesticidal activities are activated by the auxiliary protein.

Amongst the pesticidal proteins of the invention a new class of insect-specific proteins could be surprisingly identified within the scope of the present invention. The said proteins, which are designated throughout this application as VIP3, can be obtained from *Bacillus spp* strains, but preferably from *Bacillus thuringiensis* strains and most preferably from *Bacillus thuringiensis* strains AB88 and AB424. The said VIPs are present mostly in the supernatants of *Bacillus* cultures amounting to at least 75% of the total in strain AB88. The VIP3 proteins are further characterized by their unique spectrum of insecticidal activity, which includes an activity against *Agrotis* and/or *Spodoptera* species, but especially a black cutworm [BCW] and/or fall

armyworm and/or beet armyworm and/or tobacco budworm and/or corn earworm activity.

Black cutworm is an agronomically important insect quite resistant to δ -endotoxins. MacIntosh et al (1990) J Invertebr Pathol 56, 258-266 report that the δ -endotoxins CryIA(b) and CryIA(c) possesses insecticidal properties against BCW with LC₅₀ of more than 80 μ g and 18 μ g/ml of diet respectively. The vip3A insecticidal proteins according to the invention provide >50% mortality when added in an amount of protein at least 10 to 500, preferably 50 to 350, and more preferably 200 to 300 fold lower than the amount of CryIA proteins needed to achieve just 50% mortality. Especially preferred within the invention are vip3A insecticidal proteins which provide 100% mortality when added in an amount of protein at least 260 fold lower than the amount of CryIA proteins needed to achieve just 50% mortality.

The vip3 insecticidal proteins according to the invention are present mostly in the supernatants of the cultures and are therefore are to be classified as secreted proteins. They preferably contain in the N-terminal sequence a number of positively charged residues followed by a hydrophobic core region and are not N-terminally processed during export.

As the other pesticidal proteins reported hereto within the scope of the invention, the VIP3 proteins can be detected in growth stages prior to sporulation establishing a further clear distinction from other proteins that belong to the δ -endotoxin family. Preferably, expression of the insect-specific protein starts during mid-log phase and continues during sporulation. Owing to the specific expression pattern in combination with the high stability of the VIP3 proteins, large amounts of the VIP3 proteins can be found in supernatants of sporulating cultures. Especially preferred are the VIP3 proteins identified in SEQ ID NO:29 and SEQ ID NO:32 and the corresponding DNA molecules comprising nucleotide sequences encoding the said proteins, but especially those DNA molecules comprising the nucleotide sequences given in SEQ ID NO:28, SEQ ID NO:30 and SEQ ID NO:31.

The pesticidal proteins of the invention can be used in combination with Bt endotoxins or other insecticidal proteins to increase insect target range. Furthermore, the use of the VIPs of the present invention in combination with Bt δ -endotoxins or other insecticidal principles of a distinct nature has particular utility for the prevention and/or management of insect resistance. Other insecticidal principles include

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protease inhibitors (both serine and cysteine types), lectins, α -amylase and peroxidase. In one preferred embodiment, expression of VIPs in a transgenic plant is accompanied by the expression of one or more Bt δ -endotoxins. This co-expression of more than one insecticidal principle in the same transgenic plant can be achieved by genetically engineering a plant to contain and express all the genes necessary. Alternatively, a plant, Parent 1, can be genetically engineered for the expression of VIPs. A second plant, Parent 2, can be genetically engineered for the expression of Bt δ -endotoxin. By crossing Parent 1 with Parent 2, progeny plants are obtained which express all the genes introduced into Parents 1 and 2. Particularly preferred Bt δ -endotoxins are those disclosed in EP-A 0618976, herein incorporated by reference.

A substantial number of cytotoxic proteins, though not all, are binary in action. Binary toxins typically consist of two protein domains, one called the A domain and the other called the B domain (see Sourcebook of Bacterial Protein Toxins, J. E. Alouf and J. H. Freer eds.(1991) Academic Press). The A domain possesses a potent cytotoxic activity. The B domain binds an external cell surface receptor before being internalized. Typically, the cytotoxic A domain must be escorted to the cytoplasm by a translocation domain. Often the A and B domains are separate polypeptides or protomers, which are associated by a protein-protein interaction or a di-sulfide bond. However, the toxin can be a single polypeptide which is proteolytically processed within the cell into two domains as in the case for *Pseudomonas* exotoxin A. In summary binary toxins typically have three important domains, a cytotoxic A domain, a receptor binding B domain and a translocation domain. The A and B domain are often associated by protein-protein interacting domains.

The receptor binding domains of the present invention are useful for delivering any protein, toxin, enzyme, transcription factor, nucleic acid, chemical or any other factor into target insects having a receptor recognized by the receptor binding domain of the binary toxins described in this patent. Similarly, since binary toxins have translocation domains which penetrate phospholipid bilayer membranes and escort cytotoxins across those membranes, such translocation domains may be useful in escorting any protein, toxin, enzyme, transcription factor, nucleic acid, chemical or any other factor across a phospholipid bilayer such as the plasma membrane or a vesicle membrane. The translocation domain may itself perforate membranes, thus having toxic or insecticidal properties. Further, all binary toxins have cytotoxic domains; such a

cytotoxic domain may be useful as a lethal protein, either alone or when delivered into any target cell(s) by any means.

Finally, since binary toxins comprised of two polypeptides often form a complex, it is likely that there are protein-protein interacting regions within the components of the binary toxins of the invention. These protein-protein interacting domains may be useful in forming associations between any combination of toxins, enzymes, transcription factors, nucleic acids, antibodies, cell binding moieties, or any other chemicals, factors, proteins or protein domains.

Toxins, enzymes, transcription factors, antibodies, cell binding moieties or other protein domains can be fused to pesticidal or auxiliary proteins by producing in frame genetic fusions which, when translated by ribosomes, would produce a fusion protein with the combined attributes of the VIP and the other component used in the fusion. Furthermore, if the protein domain fused to the VIP has an affinity for another protein, nucleic acid, carbohydrate, lipid, or other chemical or factor, then a three-component complex can be formed. This complex will have the attributes of all of its components. A similar rationale can be used for producing four or more component complexes. These complexes are useful as insecticidal toxins, pharmaceuticals, laboratory reagents, and diagnostic reagents, etc. Examples where such complexes are currently used are fusion toxins for potential cancer therapies, reagents in ELISA assays and immunoblot analysis.

One strategy of altering pesticidal or auxiliary proteins is to fuse a 15-amino-acid "S-tag" to the protein without destroying the insect cell binding domain(s), translocation domains or protein-protein interacting domains of the proteins. The S-tag has a high affinity ($K_d = 10^{-9}$ M) for a ribonuclease S-protein, which, when bound to the S-tag, forms an active ribonuclease (See F. M. Richards and H. W. Wyckoff (1971) in "The Enzymes", Vol. IV (Boyer, P.D. ed.), pp. 647-806. Academic Press, New York). The fusion can be made in such a way as to destroy or remove the cytotoxic activity of the pesticidal or auxiliary protein, thereby replacing the VIP cytotoxic activity with a new cytotoxic ribonuclease activity. The final toxin would be comprised of the S-protein, a pesticidal protein and an auxiliary protein, where either the pesticidal protein or the auxiliary protein is produced as translational fusions with the S-tag. Similar strategies can be used to fuse other potential cytotoxins to pesticidal or auxiliary proteins including (but not limited to) ribosome inactivating

proteins, insect hormones, hormone receptors, transcription factors, proteases, phosphatases, *Pseudomonas* exotoxin A, or any other protein or chemical factor that is lethal when delivered into cells. Similarly, proteins can be delivered into cells which are not lethal, but might alter cellular biochemistry or physiology.

The spectrum of toxicity toward different species can be altered by fusing domains to pesticidal or auxiliary proteins which recognize cell surface receptors from other species. Such domains might include (but are not limited to) antibodies, transferrin, hormones, or peptide sequences isolated from phage displayed affinity selectable libraries. Also, peptide sequences which are bound to nutrients, vitamins, hormones, or other chemicals that are transported into cells could be used to alter the spectrum of toxicity. Similarly, any other protein or chemical which binds a cell surface receptor or the membrane and could be internalized might be used to alter the spectrum of activity of VIP1 and VIP2.

The pesticidal proteins of the present invention are those proteins which confer a specific pesticidal property. Such proteins may vary in molecular weight, having component polypeptides at least a molecular weight of 30 kDa or greater, preferably about 50 kDa or greater.

The auxiliary proteins of the invention may vary in molecular weight, having at least a molecular weight of about 15 kDa or greater, preferably about 20 kDa or greater; more preferably, about 30 kDa or greater. The auxiliary proteins themselves may have component polypeptides.

It is possible that the pesticidal protein and the auxiliary protein may be components of a multimeric, pesticidal protein. Such a pesticidal protein which includes the auxiliary proteins as one or more of its component polypeptides may vary in molecular weight, having at least a molecular weight of 50 kDa up to at least 200 kDa, preferably about 100 kDa to 150 kDa.

An auxiliary protein may be used in combination with the pesticidal proteins of the invention to enhance activity or to activate the pesticidal protein. To determine whether the auxiliary protein will affect activity, the pesticidal protein can be expressed alone and in combination with the auxiliary protein and the respective activities compared in feeding assays for pesticidal activity.

It may be beneficial to screen strains for potential pesticidal activity by testing activity of the strain alone and in combination with the auxiliary protein. In some

instances an auxiliary protein in combination with the native proteins of the strains yields pesticidal activity where none is seen in the absence of an auxiliary protein.

The auxiliary protein can be modified, as described above, by various methods known in the art. Therefore, for purposes of the invention, the term "Vegetative Insecticidal Protein" (VIP) encompasses those proteins produced during vegetative growth which alone or in combination can be used for pesticidal activity. This includes pesticidal proteins, auxiliary proteins and those proteins which demonstrate activity only in the presence of the auxiliary protein or the polypeptide components of these proteins.

It is recognized that there are alternative methods available to obtain the nucleotide and amino acid sequences of the present proteins. For example, to obtain the nucleotide sequence encoding the pesticidal protein, cosmid clones, which express the pesticidal protein, can be isolated from a genomic library. From larger active cosmid clones, smaller subclones can be made and tested for activity. In this manner, clones which express an active pesticidal protein can be sequenced to determine the nucleotide sequence of the gene. Then, an amino acid sequence can be deduced for the protein. For general molecular methods, see, for example, *Molecular Cloning, A Laboratory Manual*, Second Edition, Vols. 1-3, Sambrook *et al.* (eds.) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989), and the references cited therein.

The present invention also encompasses nucleotide sequences from organisms other than *Bacillus*, where the nucleotide sequences are isolatable by hybridization with the *Bacillus* nucleotide sequences of the invention. Proteins encoded by such nucleotide sequences can be tested for pesticidal activity. The invention also encompasses the proteins encoded by the nucleotide sequences. Furthermore, the invention encompasses proteins obtained from organisms other than *Bacillus* wherein the protein cross-reacts with antibodies raised against the proteins of the invention. Again the isolated proteins can be assayed for pesticidal activity by the methods disclosed herein or others well-known in the art.

Once the nucleotide sequences encoding the pesticidal proteins of the invention have been isolated, they can be manipulated and used to express the protein in a variety of hosts including other organisms, including microorganisms and plants.

The pesticidal genes of the invention can be optimized for enhanced expression in plants. See, for example EP-A 0618976; EP-A 0359472; EP-A 0385962; WO 91/16432; Perlak *et al.* (1991) Proc. Natl. Acad. Sci. USA 88:3324-3328; and Murray *et al.* (1989) Nucleic Acids Research 17: 477-498. In this manner, the genes can be synthesized utilizing plant preferred codons. That is the preferred codon for a particular host is the single codon which most frequently encodes that amino acid in that host. The maize preferred codon, for example, for a particular amino acid may be derived from known gene sequences from maize. Maize codon usage for 28 genes from maize plants is found in Murray *et al.* (1989), Nucleic Acids Research 17:477-498, the disclosure of which is incorporated herein by reference. Synthetic genes can also be made based on the distribution of codons a particular host uses for a particular amino acid.

In this manner, the nucleotide sequences can be optimized for expression in any plant. It is recognized that all or any part of the gene sequence may be optimized or synthetic. That is, synthetic or partially optimized sequences may also be used.

In like manner, the nucleotide sequences can be optimized for expression in any microorganism. For *Bacillus* preferred codon usage, see, for example US Patent No. 5,024,837 and Johansen *et al.* (1988) Gene 65:293-304.

Methodologies for the construction of plant expression cassettes as well as the introduction of foreign DNA into plants are described in the art. Such expression cassettes may include promoters, terminators, enhancers, leader sequences, introns and other regulatory sequences operably linked to the pesticidal protein coding sequence. It is further recognized that promoters or terminators of the VIP genes can be used in expression cassettes.

Generally, for the introduction of foreign DNA into plants Ti plasmid vectors have been utilized for the delivery of foreign DNA as well as direct DNA uptake, liposomes, electroporation, micro-injection, and the use of microprojectiles. Such methods had been published in the art. See, for example, Guerche *et al.*, (1987) Plant Science 52:111-116; Neuhauser *et al.*, (1987) Theor. Appl. Genet. 75:30-36; Klein *et al.*, (1987) Nature 327: 70-73; Howell *et al.*, (1980) Science 208:1265; Horsch *et al.*, (1985) Science 227: 1229-1231; DeBlock *et al.*, (1989) Plant Physiology 91:694-701; Methods for Plant Molecular Biology (Weissbach and Weissbach, eds.) Academic Press, Inc. (1988); and Methods in Plant Molecular Biology (Schuler and Zielinski,

eds.) Academic Press, Inc. (1989). See also US patent application serial no. 08/008,374 herein incorporated by reference. See also, EP-A 0193259 and EP-A 0451878. It is understood that the method of transformation will depend upon the plant cell to be transformed.

It is further recognized that the components of the expression cassette may be modified to increase expression. For example, truncated sequences, nucleotide substitutions or other modifications may be employed. See, for example Perlak *et al.* (1991) Proc. Natl. Acad. Sci. USA 88:3324-3328; Murray *et al.*, (1989) Nucleic Acids Research 17:477-498; and WO 91/16432.

The construct may also include any other necessary regulators such as terminators, (Guerineau *et al.*, (1991), Mol. Gen. Genet., 226:141-144; Proudfoot, (1991), Cell, 64:671-674; Sanfacon *et al.*, (1991), Genes Dev., 5:141-149; Mogen *et al.*, (1990), Plant Cell, 2:1261-1272; Munroe *et al.*, (1990), Gene, 91:151-158; Ballas *et al et al.*, (1989), Nucleic Acids Res., 17:7891-7903; Joshi *et al.*, (1987), Nucleic Acid Res., 15:9627-9639); plant translational consensus sequences (Joshi, C.P., (1987), Nucleic Acids Research, 15:6643-6653), introns (Luehrsen and Walbot, (1991), Mol. Gen. Genet., 225:81-93) and the like, operably linked to the nucleotide sequence. It may be beneficial to include 5' leader sequences in the expression cassette construct. Such leader sequences can act to enhance translation.

Translational leaders are known in the art and include:

Picornavirus leaders, for example, EMCV leader (encephalomyocarditis 5' noncoding region) (Elroy-Stein, O., Fuerst, T.R., and Moss, B. (1989) PNAS USA 86:6126-6130);

Potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Allison *et al.*, (1986); MDMV leader (Maize Dwarf Mosaic Virus); Virology, 154:9-20), and

Human immunoglobulin heavy-chain binding protein (BiP), (Macejak, D.G., and Sarnow, P., (1991), Nature, 353:90-94;

Untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4), (Jobling, S.A., and Gehrke, L., (1987), Nature, 325:622-625;

Tobacco mosaic virus leader (TMV), (Gallie, D.R. *et al.*, (1989), Molecular Biology of RNA, pages 237-256; and

Maize Chlorotic Mottle Virus leader (MCMV) (Lommel, S.A. *et al.*, (1991), Virology, 81:382-385. See also, Della-Cioppa *et al.*, (1987), Plant Physiology, 84:965-968.

A plant terminator may be utilized in the expression cassette. See, Rosenberg *et al.*, (1987), Gene, 56:125; Guerineau *et al.*, (1991), Mol. Gen. Genet., 226:141-144; Proudfoot, (1991), Cell, 64:671-674; Sanfacon *et al.*, (1991), Genes Dev., 5:141-149; Mogen *et al.*, (1990), Plant Cell, 2:1261-1272; Munroe *et al.*, (1990), Gene, 91:151-158; Ballas *et al.*, (1989), Nucleic Acids Res., 17:7891-7903; Joshi *et al.*, (1987), Nucleic Acid Res., 15:9627-9639.

For tissue specific expression, the nucleotide sequences of the invention can be operably linked to tissue specific promoters. See, for example, EP-A 0618976, herein incorporated by reference.

Further comprised within the scope of the present invention are transgenic plants, in particular transgenic fertile plants transformed by means of the aforescribed processes and their asexual and/or sexual progeny, which comprise and preferably also express the pesticidal protein according to the invention. Especially preferred are hybrid plants.

The transgenic plant according to the invention may be a dicotyledonous or a monocotyledonous plant. Preferred are monocotyledonous plants of the *Graminaceae* family involving Lolium, Zea, Triticum, Triticale, Sorghum, Saccharum, Bromus, Oryzae, Avena, Hordeum, Secale and Setaria plants.

Especially preferred are transgenic maize, wheat, barley, sorghum, rye, oats, turf grasses and rice.

Among the dicotyledonous plants soybean, cotton, tobacco, sugar beet, oilseed rape, and sunflower are especially preferred herein.

The expression 'progeny' is understood to embrace both, "asexually" and "sexually" generated progeny of transgenic plants. This definition is also meant to include all mutants and variants obtainable by means of known processes, such as for example cell fusion or mutant selection and which still exhibit the characteristic properties of the initially transformed parent plant, together with all crossing and fusion products of the transformed plant material.

Another object of the invention concerns the proliferation material of transgenic plants.

The proliferation material of transgenic plants is defined relative to the invention as any plant material that may be propagated sexually or asexually *in vivo* or *in vitro*. Particularly preferred within the scope of the present invention are protoplasts, cells,

calli, tissues, organs, seeds, embryos; pollen, egg cells, zygotes, together with any other propagating material obtained from transgenic plants.

Parts of plants, such as for example flowers, stems, fruits, leaves, roots originating in transgenic plants or their progeny previously transformed by means of the process of the invention and therefore consisting at least in part of transgenic cells, are also an object of the present invention.

Before the plant propagation material [fruit, tuber, grains, seed], but especially seed is sold as a commercial product, it is customarily treated with a protectant coating comprising herbicides, insecticides, fungicides, bactericides, nematocides, molluscicides or mixtures of several of these preparations, if desired together with further carriers, surfactants or application-promoting adjuvants customarily employed in the art of formulation to provide protection against damage caused by bacterial, fungal or animal pests.

In order to treat the seed, the protectant coating may be applied to the seeds either by impregnating the tubers or grains with a liquid formulation or by coating them with a combined wet or dry formulation. In addition, in special cases, other methods of application to plants are possible, eg treatment directed at the buds or the fruit.

The plant seed according to the invention comprising a DNA molecule comprising a nucleotide sequence encoding a pesticidal protein according to the invention may be treated with a seed protectant coating comprising a seed treatment compound, such as, for example, captan, carboxin, thiram (TMTD®), methalaxyl (Apron®) and pirimiphos-methyl (Actellic®) and others that are commonly used in seed treatment. Preferred within the scope of the invention are seed protectant coatings comprising an entomocidal composition according to the invention alone or in combination with one of the a seed protectant coating customarily used in seed treatment.

It is thus a further object of the present invention to provide plant propagation material for cultivated plants, but especially plant seed that is treated with a seed protectant coating as defined hereinbefore.

It is recognized that the genes encoding the pesticidal proteins can be used to transform insect pathogenic organisms. Such organisms include Baculoviruses, fungi, protozoa, bacteria and nematodes.

The *Bacillus* strains of the invention may be used for protecting agricultural crops and products from pests. Alternatively, a gene encoding the pesticide may be

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introduced via a suitable vector into a microbial host, and said host applied to the environment or plants or animals. Microorganism hosts may be selected which are known to occupy the "phytosphere" (phylloplane, phyllosphere, rhizosphere, and/or rhizoplane) of one or more crops of interest. These microorganisms are selected so as to be capable of successfully competing in the particular environment with the wild-type microorganisms, provide for stable maintenance and expression of the gene expressing the polypeptide pesticide, and, desirably, provide for improved protection of the pesticide from environmental degradation and inactivation.

Such microorganisms include bacteria, algae, and fungi. Of particular interest are microorganisms, such as bacteria, e.g., *Pseudomonas*, *Erwinia*, *Serratia*, *Klebsiella*, *Xanthomonas*, *Streptomyces*, *Rhizobium*, *Rhodopseudomonas*, *Methylius*, *Agrobacterium*, *Acetobacter*, *Lactobacillus*, *Arthrobacter*, *Azotobacter*, *Leuconostoc*, and *Alcaligenes*; fungi, particularly yeast, e.g., *Saccharomyces*, *Cryptococcus*, *Kluyveromyces*, *Sporobolomyces*, *Rhodotorula*, and *Aureobasidium*. Of particular interest are such phytosphere bacterial species as *Pseudomonas syringae*, *Pseudomonas fluorescens*, *Serratia marcescens*, *Acetobacter xylinum*, *Agrobacteria*, *Rhodopseudomonas spheroides*, *Xanthomonas campestris*, *Rhizobium melioli*, *Alcaligenes entrophus*, *Clavibacter xyli* and *Azotobacter vinlandii*, and phytosphere yeast species such as *Rhodotorula rubra*, *R. glutinis*, *R. marina*, *R. aurantiaca*, *Cryptococcus albidus*, *C. diffluens*, *C. laurentii*, *Saccharomyces rosei*, *S. pretoriensis*, *S. cerevisiae*, *Sporobolomyces rosues*, *S. odoratus*, *Kluyveromyces veronae*, and *Aureobasidium pollulans*. Of particular interest are the pigmented microorganisms.

A number of ways are available for introducing a gene expressing the pesticidal protein into the microorganism host under conditions which allow for stable maintenance and expression of the gene. For example, expression cassettes can be constructed which include the DNA constructs of interest operably linked with the transcriptional and translational regulatory signals for expression of the DNA constructs, and a DNA sequence homologous with a sequence in the host organism, whereby integration will occur, and/or a replication system which is functional in the host, whereby integration or stable maintenance will occur.

Transcriptional and translational regulatory signals include but are not limited to promoter, transcriptional initiation start site, operators, activators, enhancers, other regulatory elements, ribosomal binding sites, an initiation codon, termination signals,

and the like. See, for example, US Patent 5,039,523; US Patent No. 4,853,331; EPO 0480762A2; Sambrook *et al.* supra; Molecular Cloning, a Laboratory Manual, Maniatis *et al.* (eds) Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1982); Advanced Bacterial Genetics, Davis *et al.* (eds.) Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1980); and the references cited therein.

Suitable host cells, where the pesticide-containing cells will be treated to prolong the activity of the toxin in the cell when the then treated cell is applied to the environment of the target pest(s), may include either prokaryotes or eukaryotes, normally being limited to those cells which do not produce substances toxic to higher organisms, such as mammals. However, organisms which produce substances toxic to higher organisms could be used, where the toxin is unstable or the level of application sufficiently low as to avoid any possibility of toxicity to a mammalian host. As hosts, of particular interest will be the prokaryotes and the lower eukaryotes, such as fungi. Illustrative prokaryotes, both Gram-negative and -positive, include *Enterobacteriaceae*, such as *Escherichia*, *Erwinia*, *Shigella*, *Salmonella*, and *Proteus*; *Bacillaceae*; *Rhizobiceae*, such as *Rhizobium*; *Spirillaceae*, such as photobacterium, *Zymomonas*, *Serratia*, *Aeromonas*, *Vibrio*, *Desulfovibrio*, *Spirillum*; *Lactobacillaceae*; *Pseudomonadaceae*, such as *Pseudomonas* and *Acetobacter*; *Azotobacteraceae* and *Nitrobacteraceae*. Among eukaryotes are fungi, such as *Phycomycetes* and *Ascomycetes*, which includes yeast, such as *Saccharomyces* and *Schizosaccharomyces*; and *Basidiomycetes* yeast, such as *Rhodotorula*, *Aureobasidium*, *Sporobolomyces*, and the like.

Characteristics of particular interest in selecting a host cell for purposes of production include ease of introducing the protein gene into the host, availability of expression systems, efficiency of expression, stability of the protein in the host, and the presence of auxiliary genetic capabilities. Characteristics of interest for use as a pesticide microcapsule include protective qualities for the pesticide, such as thick cell walls, pigmentation, and intracellular packaging or formation of inclusion bodies; leaf affinity; lack of mammalian toxicity; attractiveness to pests for ingestion; ease of killing and fixing without damage to the toxin; and the like. Other considerations include ease of formulation and handling, economics, storage stability, and the like.

Host organisms of particular interest include yeast, such as *Rhodotorula sp.*, *Aureobasidium sp.*, *Saccharomyces sp.*, and *Sporobolomyces sp.*; phylloplane

organisms such as *Pseudomonas* sp., *Erwinia* sp., and *Flavobacterium* sp.; or such other organisms as *Escherichia*, *LactoBacillus* sp., *Bacillus* sp., and the like. Specific organisms include *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, *Saccharomyces cerevisiae*, *Bacillus thuringiensis*, *Escherichia coli*, *Bacillus subtilis*, and the like.

VIP genes can be introduced into micro-organisms that multiply on plants (epiphytes) to deliver VIP proteins to potential target pests. Epiphytes can be gram-positive or gram-negative bacteria for example.

Root colonizing bacteria, for example, can be isolated from the plant of interest by methods known in the art. Specifically, a *Bacillus cereus* strain which colonizes roots could be isolated from roots of a plant (for example see J. Handelsman, S. Raffel, E. Mester, L. Wunderlich and C. Grau, Appl. Environ. Microbiol. 56:713-718, (1990)). VIP1 and/or VIP2 and/or VIP3 could be introduced into a root colonizing *Bacillus cereus* by standard methods known in the art.

Specifically, VIP1 and/or VIP2 derived from *Bacillus cereus* strain AB78 can be introduced into a root colonizing *Bacillus cereus* by means of conjugation using standard methods (J. Gonzalez, B. Brown and B. Carlton, Proc. Natl. Acad. Sci. 79:6951-6955, (1982)).

Also, VIP1 and/or VIP2 and/or VIP3 or other VIPs of the invention can be introduced into the root colonizing *Bacillus* by means of electro-transformation. Specifically, VIPs can be cloned into a shuttle vector, for example, pHT3101 (D. Lereclus *et al.*, FEMS Microbiol. Letts., 60:211-218 (1989)) as described in Example 10. The shuttle vector pHT3101 containing the coding sequence for the particular VIP can then be transformed into the root colonizing *Bacillus* by means of electroporation (D. Lereclus *et al.* 1989, FEMS Microbiol. Letts. 60:211-218).

Expression systems can be designed so that VIP proteins are secreted outside the cytoplasm of gram negative bacteria, *E. coli*, for example. Advantages of having VIP proteins secreted are (1) it avoids potential toxic effects of VIP proteins expressed within the cytoplasm and (2) it can increase the level of VIP protein expressed and (3) can aid in efficient purification of VIP protein.

VIP proteins can be made to be secreted in *E. coli*, for example, by fusing an appropriate *E. coli* signal peptide to the amino-terminal end of the VIP signal peptide or replacing the VIP signal peptide with the *E. coli* signal peptide. Signal peptides

recognized by *E. coli* can be found in proteins already known to be secreted in *E. coli*, for example the OmpA protein (J. Ghrayeb, H. Kimura, M. Takahara, Y. Masui and M. Inouye, EMBO J., 3:2437-2442 (1984)). OmpA is a major protein of the *E. coli* outer membrane and thus its signal peptide is thought to be efficient in the translocation process. Also, the OmpA signal peptide does not need to be modified before processing as may be the case for other signal peptides, for example lipoprotein signal peptide

(G. Duffaud, P. March and M. Inouye, Methods in Enzymology, 153:492 (1987)).

Specifically, unique BamHI restriction sites can be introduced at the amino-terminal and carboxy-terminal ends of the VIP coding sequences using standard methods known in the art. These BamHI fragments can be cloned, in frame, into the vector pIN-III-ompA1, A2 or A3 (J. Ghrayeb, H. Kimura, M. Takahara, H. Hsiung, Y. Masui and M. Inouye, EMBO J., 3:2437-2442 (1984)) thereby creating ompA:VIP fusion gene which is secreted into the periplasmic space. The other restriction sites in the polylinker of pIN-III-ompA can be eliminated by standard methods known in the art so that the VIP amino-terminal amino acid coding sequence is directly after the ompA signal peptide cleavage site. Thus, the secreted VIP sequence in *E. coli* would then be identical to the native VIP sequence.

When the VIP native signal peptide is not needed for proper folding of the mature protein, such signal sequences can be removed and replaced with the ompA signal sequence. Unique BamHI restriction sites can be introduced at the amino-termini of the proprotein coding sequences directly after the signal peptide coding sequences of VIP and at the carboxy-termini of VIP coding sequence. These BamHI fragments can then be cloned into the pIN-III-ompA vectors as described above.

General methods for employing the strains of the invention in pesticide control or in engineering other organisms as pesticidal agents are known in the art. See, for example US Patent No. 5,039,523 and EP 0480762A2.

VIPs can be fermented in a bacterial host and the resulting bacteria processed and used as a microbial spray in the same manner that *Bacillus thuringiensis* strains have been used as insecticidal sprays. In the case of a VIP(s) which is secreted from *Bacillus*, the secretion signal is removed or mutated using procedures known in the art. Such mutations and/or deletions prevent secretion of the VIP protein(s) into the growth medium during the fermentation process. The VIPs are retained within the cell

and the cells are then processed to yield the encapsulated VIPs. Any suitable microorganism can be used for this purpose. *Pseudomonas* has been used to express *Bacillus thuringiensis* endotoxins as encapsulated proteins and the resulting cells processed and sprayed as an insecticide. (H. Gaertner *et al.* 1993, In *Advanced Engineered Pesticides*, L. Kim ed.)

Various strains of *Bacillus thuringiensis* are used in this manner. Such *Bt* strains produce endotoxin protein(s) as well as VIPs. Alternatively, such strains can produce only VIPs. A sporulation deficient strain of *Bacillus subtilis* has been shown to produce high levels of the CryIIIA endotoxin from *Bacillus thuringiensis* (Agaisse, H. and Lereclus, D., "Expression in *Bacillus subtilis* of the *Bacillus thuringiensis* CryIIIA toxin gene is not dependent on a sporulation-specific sigma factor and is increased in a *spoOA* mutant", *J. Bacteriol.* 176:4734-4741 (1994)). A similar *spoOA* mutant can be prepared in *Bacillus thuringiensis* and used to produce encapsulated VIPs which are not secreted into the medium but are retained within the cell.

To have VIPs maintained within the *Bacillus* cell the signal peptide can be disarmed so that it no longer functions as a secretion signal. Specifically, the putative signal peptide for VIP1 encompasses the first 31 amino acids of the protein with the putative consensus cleavage site, Ala-X-Ala, at the C-terminal portion of this sequence (G. von Heijne, *J. Mol. Biol.* 184:99-105 (1989)) and the putative signal peptide for VIP2 encompasses the first 40 amino acids of the protein with the putative cleavage site after Ala40. The cleavage sites in either VIP1 or VIP2 can be mutated with methods known in the art to replace the cleavage site consensus sequence with alternative amino acids that are not recognized by the signal peptidases.

Alternatively, the signal peptides of VIP1, VIP2 and/or other VIPs of the invention can be eliminated from the sequence thereby making them unrecognizable as secretion proteins in *Bacillus*. Specifically, a methionine start site can be engineered in front of the proprotein sequence in VIP1, starting at Asp32, or the proprotein sequence in VIP2, starting at Glu41 using methods known in the art.

VIP genes can be introduced into micro-organisms that multiply on plants (epiphytes) to deliver VIP proteins to potential target pests. Epiphytes can be gram-positive or gram-negative bacteria for example.

The *Bacillus* strains of the invention or the microorganisms which have been genetically altered to contain the pesticidal gene and protein may be used for

protecting agricultural crops and products from pests. In one aspect of the invention, whole, i.e., unlysed, cells of a toxin (pesticide)-producing organism are treated with reagents that prolong the activity of the toxin produced in the cell when the cell is applied to the environment of target pest(s).

Alternatively, the pesticides are produced by introducing a heterologous gene into a cellular host. Expression of the heterologous gene results, directly or indirectly, in the intracellular production and maintenance of the pesticide. These cells are then treated under conditions that prolong the activity of the toxin produced in the cell when the cell is applied to the environment of target pest(s). The resulting product retains the toxicity of the toxin. These naturally encapsulated pesticides may then be formulated in accordance with conventional techniques for application to the environment hosting a target pest, e.g., soil, water, and foliage of plants. See, for example EPA 0192319, and the references cited therein.

The active ingredients of the present invention are normally applied in the form of compositions and can be applied to the crop area or plant to be treated, simultaneously or in succession, with other compounds. These compounds can be both fertilizers or micronutrient donors or other preparations that influence plant growth. They can also be selective herbicides, insecticides, fungicides, bactericides, nematocides, molluscicides or mixtures of several of these preparations, if desired, together with further agriculturally acceptable carriers, surfactants or application-promoting adjuvants customarily employed in the art of formulation. Suitable carriers and adjuvants can be solid or liquid and correspond to the substances ordinarily employed in formulation technology, e.g. natural or regenerated mineral substances, solvents, dispersants, wetting agents, tackifiers, binders or fertilizers.

Preferred methods of applying an active ingredient of the present invention or an agrochemical composition of the present invention which contains at least one of the insect-specific proteins produced by the bacterial strains of the present invention are leaf application, seed coating and soil application. The number of applications and the rate of application depend on the intensity of infestation by the corresponding pest.

The present invention thus further provides an entomocidal composition comprising as an active ingredient at least one of the novel insect-specific proteins

according to the invention and/or a recombinant microorganism containing at least one DNA molecule comprising a nucleotide sequence encoding the novel insect-specific proteins in recombinant form, but especially a recombinant *Bacillus spp* strain, such as *Bacillus cereus* or *Bacillus thuringiensis*, containing at least one DNA molecule comprising a nucleotide sequence encoding the novel insect-specific proteins in recombinant form, or a derivative or mutant thereof, together with an agricultural adjuvant such as a carrier, diluent, surfactant or application-promoting adjuvant. The composition may also contain a further biologically active compound. The said compound can be both a fertilizer or micronutrient donor or other preparations that influence plant growth. It can also be a selective herbicide, insecticide, fungicide, bactericide, nematocide, molluscicide or mixtures of several of these preparations, if desired, together with further agriculturally acceptable carriers, surfactants or application-promoting adjuvants customarily employed in the art of formulation. Suitable carriers and adjuvants can be solid or liquid and correspond to the substances ordinarily employed in formulation technology, e.g. natural or regenerated mineral substances, solvents, dispersants, wetting agents, tackifiers, binders or fertilizers

The composition may comprise from 0.1 to 99% by weight of the active ingredient, from 1 to 99.9% by weight of a solid or liquid adjuvant, and from 0 to 25% by weight of a surfactant. The active ingredient comprising at least one of the novel insect-specific proteins according to the invention or a recombinant microorganism containing at least one DNA molecule comprising a nucleotide sequence encoding the novel insect-specific proteins in recombinant form, but especially a recombinant *Bacillus spp strain*, such as *Bacillus cereus* or *Bacillus thuringiensis* strain containing at least one DNA molecule comprising a nucleotide sequence encoding the novel insect-specific proteins in recombinant form, or a derivative or mutant thereof, or the composition containing the said active ingredient, may be administered to the plants or crops to be protected together with certain other insecticides or chemicals (1993 Crop Protection Chemicals Reference, Chemical and Pharmaceutical Press, Canada) without loss of potency. It is compatible with most other commonly used agricultural spray materials but should not be used in extremely alkaline spray solutions. It may be administered as a dust, a suspension, a wettable powder or in any other material form suitable for agricultural application.

The invention further provides methods for controlling or inhibiting of insect pests by applying an active ingredient comprising at least one of the novel insect-specific proteins according to the invention or a recombinant microorganism containing at least one DNA molecule comprising a nucleotide sequence encoding the novel insect-specific proteins in recombinant form or a composition comprising the said active ingredient to (a) an environment in which the insect pest may occur, (b) a plant or plant part in order to protect said plant or plant part from damage caused by an insect pest, or (c) seed in order to protect a plant which develops from said seed from damage caused by an insect pest.

A preferred method of application in the area of plant protection is application to the foliage of the plants (foliar application), with the number of applications and the rate of application depending on the plant to be protected and the risk of infestation by the pest in question. However, the active ingredient may also penetrate the plants through the roots (systemic action) if the locus of the plants is impregnated with a liquid formulation or if the active ingredient is incorporated in solid form into the locus of the plants, for example into the soil, e.g. in granular form (soil application). In paddy rice crops, such granules may be applied in metered amounts to the flooded rice field.

The compositions according to the invention are also suitable for protecting plant propagating material, e.g. seed, such as fruit, tubers or grains, or plant cuttings, from insect pests. The propagation material can be treated with the formulation before planting: seed, for example, can be dressed before being sown. The active ingredient of the invention can also be applied to grains (coating), either by impregnating the grains with a liquid formulation or by coating them with a solid formulation. The formulation can also be applied to the planting site when the propagating material is being planted, for example to the seed furrow during sowing. The invention relates also to those methods of treating plant propagation material and to the plant propagation material thus treated.

The compositions according to the invention comprising as an active ingredient a recombinant microorganism containing at least one of the novel toxin genes in recombinant form, but especially a recombinant *Bacillus spp strain, such as Bacillus cereus or Bacillus thuringiensis* strain containing at least one DNA molecule comprising a nucleotide sequence encoding the novel insect-specific proteins in recombinant form, or a derivative or mutant thereof may be applied in any method

known for treatment of seed or soil with bacterial strains. For example, see US Patent No. 4,863,866. The strains are effective for biocontrol even if the microorganism is not living. Preferred is, however, the application of the living microorganism.

Target crops to be protected within the scope of the present invention comprise, e.g., the following species of plants:

cereals (wheat, barley, rye, oats, rice, sorghum and related crops), beet (sugar beet and fodder beet), forage grasses (orchardgrass, fescue, and the like), drupes, pomes and soft fruit (apples, pears, plums, peaches, almonds, cherries, strawberries, raspberries and blackberries), leguminous plants (beans, lentils, peas, soybeans), oil plants (rape, mustard, poppy, olives, sunflowers, coconuts, castor oil plants, cocoa beans, groundnuts), cucumber plants (cucumber, marrows, melons) fiber plants (cotton, flax, hemp, jute), citrus fruit (oranges, lemons, grapefruit, mandarins), vegetables (spinach, lettuce, asparagus, cabbages and other Brassicae, onions, tomatoes, potatoes, paprika), lauraceae (avocados, carrots, cinnamon, camphor), deciduous trees and conifers (e.g. linden-trees, yew-trees, oak-trees, alders, poplars, birch-trees, firs, larches, pines), or plants such as maize, tobacco, nuts, coffee, sugar cane, tea, vines, hops, bananas and natural rubber plants, as well as ornamentals (including composites).

A recombinant *Bacillus* spp strain, such as *Bacillus cereus* or *Bacillus thuringiensis* strain, containing at least one DNA molecule comprising a nucleotide sequence encoding the novel insect-specific proteins in recombinant form is normally applied in the form of entomocidal compositions and can be applied to the crop area or plant to be treated, simultaneously or in succession, with further biologically active compounds. These compounds may be both fertilizers or micronutrient donors or other preparations that influence plant growth. They may also be selective herbicides, insecticides, fungicides, bactericides, nematocides, molluscicides or mixtures of several of these preparations, if desired together with further carriers, surfactants or application-promoting adjuvants customarily employed in the art of formulation.

The active ingredient according to the invention may be used in unmodified form or together with any suitable agriculturally acceptable carrier. Such carriers are adjuvants conventionally employed in the art of agricultural formulation, and are therefore formulated in known manner to emulsifiable concentrates, coatable pastes, directly sprayable or dilutable solutions, dilute emulsions, wettable powders, soluble powders,

dusts, granulates, and also encapsulations, for example, in polymer substances. Like the nature of the compositions, the methods of application, such as spraying, atomizing, dusting, scattering or pouring, are chosen in accordance with the intended objective and the prevailing circumstances. Advantageous rates of application are normally from about 50 g to about 5 kg of active ingredient (a.i.) per hectare ("ha", approximately 2.471 acres), preferably from about 100 g to about 2kg a.i./ha. Important rates of application are about 200 g to about 1kg a.i./ha and 200g to 500g a.i./ha.

For seed dressing advantageous application rates are 0.5 g to 1000 g a.i. per 100 kg seed, preferably 3 g to 100 g a.i. per 100 kg seed or 10 g to 50 g a.i. per 100 kg seed.

Suitable carriers and adjuvants can be solid or liquid and correspond to the substances ordinarily employed in formulation technology, e.g. natural or regenerated mineral substances, solvents, dispersants, wetting agents, tackifiers, binders or fertilizers. The formulations, i.e. the entomocidal compositions, preparations or mixtures containing the recombinant *Bacillus spp* strain, such as *Bacillus cereus* or *Bacillus thuringiensis* strain containing at least one DNA molecule comprising a nucleotide sequence encoding the novel insect-specific proteins in recombinant form as an active ingredient or combinations thereof with other active ingredients, and, where appropriate, a solid or liquid adjuvant, are prepared in known manner, e.g., by homogeneously mixing and/or grinding the active ingredients with extenders, e.g., solvents, solid carriers, and in some cases surface-active compounds (surfactants).

Suitable solvents are: aromatic hydrocarbons, preferably the fractions containing 8 to 12 carbon atoms, e.g. xylene mixtures or substituted naphthalenes, phthalates such as dibutyl phthalate or dioctyl phthalate, aliphatic hydrocarbons such as cyclohexane or paraffins, alcohols and glycols and their ethers and esters, such as ethanol, ethylene glycol monomethyl or monoethyl ether, ketones such as cyclohexanone, strongly polar solvents such as N-methyl-2-pyrrolidone, dimethylsulfoxide or dimethylformamide, as well as vegetable oils or epoxidised vegetable oils such as epoxidised coconut oil or soybean oil; or water.

The solid carriers used, e.g., for dusts and dispersible powders, are normally natural mineral fillers such as calcite, talcum, kaolin, montmorillonite or attapulgite. In order to improve the physical properties it is also possible to add highly dispersed silicic acid or highly dispersed absorbent polymers. Suitable granulated adsorptive

carriers are porous types, for example pumice, broken brick, sepiolite or bentonite; and suitable nonsorbent carriers are materials such as calcite or sand. In addition, a great number of pregranulated materials of inorganic or organic nature can be used, e.g. especially dolomite or pulverized plant residues.

Depending on the nature of the active ingredients to be formulated, suitable surface-active compounds are non-ionic, cationic and/or anionic surfactants having good emulsifying, dispersing and wetting properties. The term "surfactants" will also be understood as comprising mixtures of surfactants. Suitable anionic surfactants can be both water-soluble soaps and water-soluble synthetic surface-active compounds. Suitable soaps are the alkali metal salts, alkaline earth metal salts or unsubstituted or substituted ammonium salts of higher fatty acids (C_{10} - C_{22}), e.g. the sodium or potassium salts of oleic or stearic acid, or of natural fatty acid mixtures which can be obtained, e.g. from coconut oil or tallow oil. Further suitable surfactants are also the fatty acid methylaurin salts as well as modified and unmodified phospholipids.

More frequently, however, so-called synthetic surfactants are used, especially fatty sulfonates, fatty sulfates, sulfonated benzimidazole derivatives or alkylarylsulfonates. The fatty sulfonates or sulfates are usually in the forms of alkali metal salts, alkaline earth metal salts or unsubstituted or substituted ammonium salts and generally contain a C_8 - C_{22} alkyl radical which also includes the alkyl moiety of acyl radicals, e.g. the sodium or calcium salt of lignosulfonic acid, of dodecylsulfate, or of a mixture of fatty alcohol sulfates obtained from natural fatty acids. These compounds also comprise the salts of sulfuric acid esters and sulfonic acids of fatty alcohol/ethylene oxide adducts. The sulfonated benzimidazole derivatives preferably contain 2 sulfonic acid groups and one fatty acid radical containing about 8 to 22 carbon atoms. Examples of alkylarylsulfonates are the sodium, calcium or triethanolamine salts of dodecylbenzenesulfonic acid, dibutyl-naphthalenesulfonic acid, or of a naphthalenesulfonic acid/formaldehyde condensation product. Also suitable are corresponding phosphates, e.g. salts of the phosphoric acid ester of an adduct of p-nonylphenol with 4 to 14 moles of ethylene oxide.

Non-ionic surfactant are preferably polyglycol ether derivatives of aliphatic or cycloaliphatic alcohols, or saturated or unsaturated fatty acids and alkylphenols, said derivatives containing 3 to 30 glycol ether groups and 8 to 20 carbon atoms in the

(aliphatic) hydrocarbon moiety and 6 to 18 carbon atoms in the alkyl moiety of the alkylphenols.

Further suitable non-ionic surfactants are the water-soluble adducts of polyethylene oxide with polypropylene glycol, ethylenediaminopolypropylene glycol and alkylpolypropylene glycol containing 1 to 10 carbon atoms in the alkyl chain, which adducts contain 20 to 250 ethylene glycol ether groups and 10 to 100 propylene glycol ether groups. These compounds usually contain 1 to 5 ethylene glycol units per propylene glycol unit. Representative examples of non-ionic surfactants are nonylphenolpolyethoxyethanols, castor oil polyglycol ethers, polypropylene/polyethylene oxide adducts, tributylphenoxypolyethoxyethanol, polyethylene glycol and octylphenoxypolyethoxyethanol. Fatty acid esters of polyoxyethylene sorbitan, such as polyoxyethylene sorbitan trioleate, are also suitable non-ionic surfactants.

Cationic surfactants are preferably quaternary ammonium salts which contain, as N-substituent, at least one C_8 - C_{22} alkyl radical and, as further substituents, lower unsubstituted or halogenated alkyl, benzyl or hydroxyl-lower alkyl radicals. The salts are preferably in the form of halides, methylsulfates or ethylsulfates, e.g., stearyltrimethylammonium chloride or benzyldi-(2-chloroethyl)ethylammonium bromide.

The surfactants customarily employed in the art of formulation are described, e.g., in "McCutcheon's Detergents and Emulsifiers Annual", MC Publishing Corp. Ridgewood, N.J., 1979; Dr. Helmut Stache, "Tensid Taschenbuch" (Handbook of Surfactants), Carl Hanser Verlag, Munich/Vienna.

Another particularly preferred characteristic of an entomocidal composition of the present invention is the persistence of the active ingredient when applied to plants and soil. Possible causes for loss of activity include inactivation by ultra-violet light, heat, leaf exudates and pH. For example, at high pH, particularly in the presence of reductant, δ -endotoxin crystals are solubilized and thus become more accessible to proteolytic inactivation. High leaf pH might also be important, particularly where the leaf surface can be in the range of pH 8-10. Formulation of an entomocidal composition of the present invention can address these problems by either including additives to help prevent loss of the active ingredient or encapsulating the material in such a way that the active ingredient is protected from inactivation. Encapsulation

can be accomplished chemically (McGuire and Shasha, J Econ Entomol 85: 1425-1433, 1992) or biologically (Barnes and Cummings, 1986; EP-A 0 192 319). Chemical encapsulation involves a process in which the active ingredient is coated with a polymer while biological encapsulation involves the expression of the δ -endotoxin genes in a microbe. For biological encapsulation, the intact microbe containing at least one DNA molecule comprising a nucleotide sequence encoding the novel insect-specific proteins in recombinant form is used as the active ingredient in the formulation. The addition of UV protectants might effectively reduce irradiation damage. Inactivation due to heat could also be controlled by including an appropriate additive.

Preferred within the present application are formulations comprising living microorganisms as active ingredient either in form of the vegetative cell or more preferable in form of spores, if available. Suitable formulations may consist, for example, of polymer gels which are crosslinked with polyvalent cations and comprise these microorganisms. This is described, for example, by D.R. Fravel et al. in *Phytopathology*, Vol. 75, No. 7, 774-777, 1985 for alginate as the polymer material. It is also known from this publication that carrier materials can be co-used. These formulations are as a rule prepared by mixing solutions of naturally occurring or synthetic gel-forming polymers, for example alginates, and aqueous salt solutions of polyvalent metal ions such that individual droplets form, it being possible for the microorganisms to be suspended in one of the two or in both reaction solutions. Gel formation starts with the mixing in drop form. Subsequent drying of these gel particles is possible. This process is called ionotropic gelling. Depending on the degree of drying, compact and hard particles of polymers which are structurally crosslinked via polyvalent cations and comprise the microorganisms and a carrier present predominantly uniformly distributed are formed. The size of the particles can be up to 5 mm.

Compositions based on partly crosslinked polysaccharides which, in addition to a microorganism, for example, can also comprise finely divided silicic acid as the carrier material, crosslinking taking place, for example, via Ca^{++} ions, are described in EP-A1-0 097 571. The compositions have a water activity of not more than 0.3. W.J. Cornick et al. describe in a review article [New Directions in Biological Control: Alternatives for Suppressing Agricultural Pests and Diseases, pages 345-372, Alan R.

Liss, Inc. (1990)] various formulation systems, granules with vermiculite as the carrier and compact alginate beads prepared by the ionotropic gelling process being mentioned. Such compositions are also disclosed by D.R.Fravel in Pesticide Formulations and Application Systems: 11th Volume, ASTM STP 1112 American Society for Testing and Materials, Philadelphia, 1992, pages 173 to 179 and can be used to formulate the recombinant microorganisms according to the invention.

The entomocidal compositions of the invention usually contain from about 0.1 to about 99%, preferably about 0.1 to about 95%, and most preferably from about 3 to about 90% of the active ingredient, from about 1 to about 99.9%, preferably from about 1 to about 99%, and most preferably from about 5 to about 95% of a solid or liquid adjuvant, and from about 0 to about 25%, preferably about 0.1 to about 25%, and most preferably from about 0.1 to about 20% of a surfactant.

In a preferred embodiment of the invention the entomocidal compositions usually contain 0.1 to 99%, preferably 0.1 to 95%, of a recombinant *Bacillus spp strain*, such as *Bacillus cereus* or *Bacillus thuringiensis* strain containing at least one DNA molecule comprising a nucleotide sequence encoding the novel insect-specific proteins in recombinant form, or combination thereof with other active ingredients, 1 to 99.9% of a solid or liquid adjuvant, and 0 to 25%, preferably 0.1 to 20%, of a surfactant.

Whereas commercial products are preferably formulated as concentrates, the end user will normally employ dilute formulations of substantially lower concentration. The entomocidal compositions may also contain further ingredients, such as stabilizers, antifoams, viscosity regulators, binders, tackifiers as well as fertilizers or other active ingredients in order to obtain special effects.

In one embodiment of the invention a *Bacillus cereus* microorganism has been isolated which is capable of killing *Diabrotica virgifera virgifera*, and *Diabrotica longicornis barberi*. The novel *B. cereus* strain AB78 has been deposited in the Agricultural Research Service, Patent Culture Collection (NRRL), Northern Regional Research Center, 1815 North University Street, Peoria, IL 61604, USA and given Accession No. NRRL B-21058.

A fraction protein has been substantially purified from the *B. cereus* strain. This purification of the protein has been verified by SDS-PAGE and biological activity. The

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protein has a molecular weight of about 60 to about 100 kDa, particularly about 70 to about 90 kDa, more particularly about 80 kDa, hereinafter VIP.

Amino-terminal sequencing has revealed the N-terminal amino-acid sequence to be:

NH₂-Lys-Arg-Glu-Ile-Asp-Glu-Asp-Thr-Asx-Gly-Asp-Ser-Ile-Pro-
(SEQ ID NO:8) where Asx represents either Asp or Asn. The entire amino acid sequence is given in SEQ ID NO:7. The DNA sequence which encodes the amino acid sequence of SEQ ID NO:7 is disclosed in SEQ ID NO:6.

An oligonucleotide probe for the region of the gene encoding amino acids 3-9 of the NH₂-terminus has been generated. The probe was synthesized based on the codon usage of a *Bacillus thuringiensis* (Bt) δ -endotoxin gene. The nucleotide sequence of the oligonucleotide probe used for Southern hybridizations was as follows:

5'- GAA ATT GAT CAA GAT ACN GAT -3' (SEQ ID NO:9)

where N represents any base.

In addition, the DNA probe for the Bc AB78 VIP1 gene described herein, permits the screening of any *Bacillus* strain or other organisms to determine whether the VIP1 gene (or related gene) is naturally present or whether a particular transformed organism includes the VIP1 gene.

The invention now being generally described, the same will be better understood by reference to the following detailed examples that are provided for the purpose of illustration and are not to be considered limiting of the invention unless so specified.

A standard nomenclature has been developed based on the sequence identity of the proteins encompassed by the present invention. The gene and protein names for the detailed examples which follow and their relationship to the names used in the parent application [US application serial no 314594/08] are shown below.

<i>Gene / Protein Name under Standard Nomenclature</i>	<i>Gene / Protein Name in Parent</i>	<i>Description of Protein</i>
VIP1A(a)	VIP1	VIP1 from strain AB78 as disclosed in SEQ ID NO:5.
VIP2A(a)	VIP2	VIP2 from strain AB78 as disclosed in SEQ ID NO:2.
VIP1A(b)	VIP1 homolog	VIP1 from <i>Bacillus thuringiensis</i> var. <i>tenebrionis</i> as disclosed in SEQ ID NO:21.
VIP2A(b)	VIP2 homolog	VIP2 from <i>Bacillus thuringiensis</i> var. <i>tenebrionis</i> as disclosed in SEQ ID NO:20.
VIP3A(a)	--	VIP from strain AB88 as disclosed in SEQ ID NO:28 of the present application
VIP3A(b)	--	VIP from strain AB424 as disclosed in SEQ ID NO:31 of the present application

EXPERIMENTALFormulation Examples

The active ingredient used in the following formulation examples are *Bacillus cereus* strain AB78 having Accession No. NRRL B-21058; *Bacillus thuringiensis* strains having Accession Nos. NRRL B-21060, NRRL B-21224, NRRL B-21225, NRRL B-21226, NRRL B-21227, and NRRL B-21439; and *Bacillus spp* strains having Accession Nos NRRL B-21228, NRRL B-21229, and NRRL B-21230. All the mentioned strains are natural isolates comprising the insect-specific proteins according to the invention.

Alternatively, the isolated insect-specific proteins are used as the active ingredient alone or in combination with the above-mentioned *Bacillus* strains.

A1. Wettable powders

	a)	b)	c)
<i>Bacillus thuringiensis</i> spores	25%	50%	75%
sodium lignosulfonate	5%	5%	--
sodium laurylsulfate	3%	--	5%
sodium diisobutyl naphthalenesulfonate	--	6%	10%
octylphenol polyethylene glycol ether (7-8 moles of ethylene oxid)	--	2%	--
highly dispersed silicid acid	5%	10%	10%
kaolin	62%	27%	--

The spores are thoroughly mixed with the adjuvants and the mixture is thoroughly ground in a suitable mill, affording wettable powders which can be diluted with water to give suspensions of the desired concentrations.

A2. Emulsifiable concentrate

<i>Bacillus thuringiensis</i> spores	10%
octylphenol polyethylene glycol ether (4-5 moles ethylene oxide)	3%
clacium dodecylbenzensulfonate	3%

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castor oil polyglycol ether (36 moles of ethylene oxide)	4%
cyclohexanone	30%
xylene mixture	50%

Emulsions of any required concentration can be obtained from this concentrate by dilution with water.

A3. Dusts

	a)	b)
<i>Bacillus thuringiensis</i> spores	5%	8%
talcum	95%	--
kaolin	--	92%

Ready for use dusts are obtained by mixing the active ingredient with the carriers and grinding the mixture in a suitable mill.

A4. Extruder Granulate

<i>Bacillus thuringiensis</i> spores	10%
sodium lignosulfonate	2%
carboxymethylcellulose	1%
kaolin	87%

The active ingredient or combination is mixed and ground with the adjuvants and the mixture is subsequently moistened with water. The mixture is extruded, granulated and the dried in a stream of air.

A5. Coated Granule

<i>Bacillus thuringiensis</i> spores	3%
polyethylene glycol (mol wt 200)	3%
kaolin	94%

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The active ingredient or combination is uniformly applied in a mixer to the kaolin moistened with polyethylene glycol. Non-dusty coated granulates are obtained in this manner.

A6. Suspension Concentrate

<i>Bacillus thuringiensis</i> spores	40%
ethylene glycol	10%
nonylphenol polyethylene glycol ether (15 moles of ethylene oxide)	6%
sodium lignosulfonate	10%
carboxymethylcellulose	1%
37% aqueous formaldehyde solution	0.2%
silicone oil in the form of a 75% aqueous solution	0.8%
water	32%

The active ingredient or combination is intimately mixed with the adjuvants giving a suspension concentrate from which suspensions of any desired concentration can be obtained by dilution with water.

EXAMPLE 1. AB78 ISOLATION AND CHARACTERIZATION

Bacillus cereus strain AB78 was isolated as a plate contaminant in the laboratory on T3 media (per liter: 3 g tryptone, 2 g tryptose, 1.5 g yeast extract, 0.05 M sodium phosphate (pH 6.8), and 0.005 g MnCl₂; Travers, R.S. 1983). During log phase growth, AB78 gave significant activity against western corn rootworm. Antibiotic activity against gram-positive *Bacillus spp.* was also demonstrated (Table 12).

TABLE 12

Antibiotic activity of AB78 culture supernatant

Bacteria tested	Zone of inhibition(cm)	
	AB78	Streptomycin
<i>E. coli</i>	0.0	3.0
<i>B. megaterium</i>	1.1	2.2
<i>B. mycoides</i>	1.3	2.1
<i>B. cereus</i> CB	1.0	2.0
<i>B. cereus</i> 11950	1.3	2.1
<i>B. cereus</i> 14579	1.0	2.4
<i>B. cereus</i> AB78	0.0	2.2
<i>Bt var. israelensis</i>	1.1	2.2
<i>Bt var. tenebrionis</i>	0.9	2.3

Morphological characteristics of AB78 are as follows:

Vegetative rods straight, 3.1-5.0 mm long and 0.5-2.0 mm wide. Cells with rounded ends, single in short chains. Single subterminal, cylindrical-oval, endospore formed per cell. No parasporal crystal formed. Colonies opaque, erose, lobate and flat. No pigments produced. Cells motile. Flagella present.

Growth characteristics of AB78 are as follows:

Facultative anaerobe with optimum growth temperature of 21-30°C. Will grow at 15, 20, 25, 30 and 37°C. Will not grow above 40°C. Grows in 5-7% NaCl.

Table 13 provides the biochemical profile of AB78.

TABLE 13
Biochemical characteristics of *B. cereus* strain AB78.

Acid from L-arabinose	-	Methylene blue reoxidized	+
Gas from L-arabinose	-	Nitrate reduced	+
Acid from D-xylose	-	NO ₃ reduced to NO ₂	+
Gas from D-xylose	-	VP	+
Acid from D-glucose	+	H ₂ O ₂ decomposed	+
Gas from D-glucose	-	Indole	-
Acid from lactose	-	Tyrosine decomposed	+
Gas from lactose	-	Dihydroxiacetone	-
Acid from sucrose	-	Litmus milk acid	-
Gas from sucrose	-	Litmus milk coagulated	-
Acid from D-mannitol	-	Litmus milk alkaline	-
Gas from D-mannitol	-	Litmus milk peptonized	-
Propionate utilization	+	Litmus milk reduced	-
Citrate utilization	+	Casein hydrolyzed	+
Hippurate hydrolysis	w	Starch hydrolyzed	+
Methylene blue reduced	+	Gelatin liquidified	+
Lecithinase produced	w		

w= weak reaction

EXAMPLE 2. BACTERIAL CULTURE

A subculture of Bc strain AB78 was used to inoculate the following medium, known as TB broth:

Tryptone	12	g/l
Yeast Extract	24	g/l
Glycerol	4	ml/l
KH ₂ PO ₄	2.1	g/l
K ₂ HPO ₄	14.7	g/l
pH 7.4		

The potassium phosphate was added to the autoclaved broth after cooling. Flasks were incubated at 30°C on a rotary shaker at 250 rpm for 24 h-36 h, which represents an early to mid-log growth phase.

The above procedure can be readily scaled up to large fermentors by procedures well known in the art.

During vegetative growth, usually 24-36 h. after starting the culture, which represents an early to mid-log growth phase, AB78 bacteria were centrifuged from the culture supernatant. The culture supernatant containing the active protein was used in bioassays.

EXAMPLE 3. INSECT BIOASSAYS

B. cereus strain AB78 was tested against various insects as described below.

Western, Northern and Southern corn rootworm, *Diabrotica virgifera virgifera*, *D. longicornis barberi* and *D. undecempunctata howardi*, respectively: dilutions were made of AB78 culture supernatant grown 24-36 h., mixed with molten artificial diet (Marrone *et al.* (1985) J. of Economic Entomology 78:290-293) and allowed to solidify. Solidified diet was cut and placed in dishes. Neonate larvae were placed on the diet and held at 30 C. Mortality was recorded after 6 days.

E. coli clone bioassay: *E. coli* cells were grown overnight in broth containing 100 µg/ml ampicillin at 37°C. Ten ml culture was sonicated 3X for 20 sec each. 500 µl of sonicated culture was added to molten western corn rootworm diet.

Colorado potato beetle, *Leptinotarsa decemlineata*: dilutions in Triton X-100 (to give final concentration of 0.1% TX-100) were made of AB78 culture supernatant grown 24-36 h. Five cm² potato leaf pieces were dipped into these dilutions, air dried, and placed on moistened filter paper in plastic dishes. Neonate larvae were placed on the leaf pieces and held at 30°C. Mortality was recorded after 3-5 days.

Yellow mealworm, *Tenebrio molitor*.. dilutions were made of AB78 culture supernatant grown 24-36 h., mixed with molten artificial diet (Bioserv #F9240) and allowed to solidify. Solidified diet was cut and placed in plastic dishes. Neonate larvae were placed on the diet and held at 30°C. Mortality was recorded after 6-8 days.

European corn borer, black cutworm, tobacco budworm, tobacco hornworm and beet armyworm; *Ostrinia nubilalis*, *Agrotis ipsilon*, *Heliothis virescens*, *Manduca sexta* and *Spodoptera exigua*, respectively: dilutions, in TX-100 (to give final concentration of 0.1% TX-100), were made of AB78 culture supernatant grown 24-36 hrs. 100 μ l was pipetted onto the surface of 18 cm² of solidified artificial diet (Bioserv #F9240) and allowed to air dry. Neonate larvae were then placed onto the surface of the diet and held at 30°C. Mortality was recorded after 3-6 days.

Northern house mosquito, *Culex pipiens*: dilutions were made of AB78 culture supernatant grown 24-36 h. 100 μ l was pipetted into 10 ml water in a 30 ml plastic cup. Third instar larvae were added to the water and held at room temperature. Mortality was recorded after 24-48 hours. The spectrum of entomocidal activity of AB78 is given in Table 14.

TABLE 14
Activity of AB78 culture supernatant against various insect species

Insect species tested to date	Order	Activity
Western corn rootworm (<i>Diabrotica virgifera</i> <i>virgifera</i>)	Col	+++
Northern corn rootworm (<i>Diabrotica longicornis</i> <i>barberi</i>)	Col	+++
Southern corn rootworm (<i>Diabrotica undecimpunctata</i> <i>howardi</i>)	Col	-
Colorado potato beetle (<i>Leptinotarsa decemlineata</i>)	Col	-
Yellow mealworm (<i>Tenebrio molitor</i>)	Col	-

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European corn borer		
(<i>Ostrinia nubilalis</i>)	Lep	-
Tobacco budworm		
(<i>Heliothis virescens</i>)	Lep	-
Tobacco hornworm		
(<i>Manduca sexta</i>)	Lep	-
Beet armyworm		
(<i>Spodoptera exigua</i>)	Lep	-
Black cutworm		
(<i>Agrotis ipsilon</i>)	Lep	-
Northern house mosquito		
(<i>Culex pipiens</i>)	Dip	-

The newly discovered *B. cereus* strain AB78 showed a significantly different spectrum of insecticidal activity as compared to known coleopteran active δ -endotoxins from Bt. In particular, AB78 showed more selective activity against beetles than known coleopteran-active Bt strains in that it was specifically active against *Diabrotica* spp. More specifically, it was most active against *D. virgifera* *virgifera* and *D. longicornis barberi* but not *D. undecimpunctata howardi*.

A number of *Bacillus* strains were bioassayed for activity during vegetative growth (Table 15) against western corn rootworm. The results demonstrate that AB78 is unique in that activity against western corn rootworm is not a general phenomenon.

TABLE 15

Activity of culture supernatants from various *Bacillus* spp. against western corn rootworm

<i>Bacillus</i> strain	Percent WCRW mortality
<i>B. cereus</i> AB78 (Bat.1)	100
<i>B. cereus</i> AB78 (Bat.2)	100
<i>B. cereus</i> (Carolina Bio.)	12
<i>B. cereus</i> ATCC 11950	12
<i>B. cereus</i> ATCC 14579	8
<i>B. mycoides</i> (Carolina Bio.)	30
<i>B. popilliae</i>	28
<i>B. thuringiensis</i> HD135	41
<i>B. thuringiensis</i> HD191	9
<i>B. thuringiensis</i> GC91	4
<i>B. thuringiensis isrealensis</i>	24
Water Control	4

Specific activity of AB78 against western corn rootworm is provided in Table 16.

TABLE 16**Activity of AB78 culture supernatant against neonate western corn rootworm**

Culture supernatant concentration (μ l/ml)	Percent WCRW mortality
100	100
25	87
10	80
5	40
2.5	20
1	6
0	0

The LC₅₀ was calculated to be 6.2 μ l of culture supernatant per ml of western corn rootworm diet.

The cell pellet was also bioassayed and had no activity against WCRW. Thus, the presence of activity only in the supernatant indicates that this VIP is an exotoxin.

EXAMPLE 4. ISOLATION AND PURIFICATION OF CORN ROOTWORM**ACTIVE PROTEINS FROM AB78.**

Culture media free of cells and debris was made to 70% saturation by the addition of solid ammonium sulfate (472 g/L). Dissolution was at room temperature followed by cooling in an ice bath and centrifugation at 10,000 X g for thirty minutes to pellet the precipitated proteins. The supernatant was discarded and the pellet was dissolved in 1/10 the original volume of 20 mM TRIS-HCl at pH 7.5. The dissolved pellet was desalted either by dialysis in 20 mM TRIS-HCl pH 7.5, or passing through a desalting column.

The desalted material was titrated to pH 3.5 using 20 mM sodium citrate pH 2.5. Following a thirty minute room temperature incubation the solution was centrifuged at

3000 X g for ten minutes. The supernatant at this stage contained the greatest amount of active protein.

Following neutralization of the pH to 7.0 the supernatant was applied to a Mono-Q, anion exchange, column equilibrated with 20 mM TRIS pH 7.5 at a flow rate of 300 mL/min. The column was developed with a stepwise and linear gradient employing 400 mM NaCl in 20 mM TRIS pH 7.5.

Bioassay of the column fractions and SDS-PAGE analysis were used to confirm the active fractions. SDS-PAGE analysis identified the biologically active protein as having components of a molecular weight in the range of about 80 kDa and 50 kDa.

EXAMPLE 5. SEQUENCE ANALYSIS OF THE CORN ROOTWORM ACTIVE PROTEIN

The 80 kDa component isolated by SDS-PAGE was transferred to PVDF membrane and was subjected to amino-terminal sequencing as performed by repetitive Edman cycles on an ABI 470 pulsed-liquid sequencer. Transfer was carried out in 10 mM CAPS buffer with 10% methanol pH 11.0 as follows:

Incubation of the gel following electrophoresis was done in transfer buffer for five minutes. ProBlott PVDF membrane was wetted with 100% MeOH briefly then equilibrated in transfer buffer. The sandwich was arranged between foam sponges and filter paper squares with the configuration of cathode-gel-membrane-anode.

Transfer was performed at 70 V constant voltage for 1 hour.

Following transfer, the membrane was rinsed with water and stained for two minutes with 0.25% Coomassie Blue R-250 in 50% MeOH.

Destaining was done with several rinses with 50% MeOH 40% water 10% acetic acid.

Following destaining the membrane was air dried prior to excision of the bands for sequence analysis. A BlottCartridge and appropriate cycles were utilized to achieve maximum efficiency and yield. Data analysis was performed using model 610 Sequence Analysis software for identifying and quantifying the PTH-amino acid derivatives for each sequential cycle.

The N-terminal sequence was determined to be:

NH₂-Lys-Arg-Glu-Ile-Asp-Glu-Asp-Thr-Asp-Thr-Asx-Gly-Asp-Ser-Ile-Pro-

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(SEQ ID NO:8) where Asx represents Asp or Asn. The complete amino acid sequence for the 80 kDa component is disclosed in SEQ ID NO:7. The DNA sequence which encodes SEQ ID NO:7 is disclosed in SEQ ID NO:6.

EXAMPLE 6. CONSTRUCTION OF DNA PROBE

An oligonucleotide probe for the region of the gene encoding amino acids 3-9 of the N-terminal sequence (Example 5) was generated. The probe was synthesized based on the codon usage of a *Bacillus thuringiensis* (Bt) δ -endotoxin gene. The nucleotide sequence

5'- GAA ATT GAT CAA GAT ACN GAT -3' (SEQ ID NO:9)

was used as a probe in Southern hybridizations. The oligonucleotide was synthesized using standard procedures and equipment.

EXAMPLE 7. ISOELECTRIC POINT DETERMINATION OF THE CORN ROOTWORM ACTIVE PROTEIN

Purified protein from step 5 of the purification process was analyzed on a 3-9 pI isoelectric focusing gel using the Phastgel electrophoresis system (Pharmacia). Standard operating procedures for the unit were followed for both the separation and silver staining development procedures. The pI was approximated at about 4.9.

EXAMPLE 8. PCR DATA ON AB78

PCR analysis (See, for example US patent application serial no. 08/008,006; and, Carozzi *et al.* (1991) Appl. Environ. Microbiol. 57(11):3057-3061, herein incorporated by reference.) was used to verify that the *B. cereus* strain AB78 did not contain any insecticidal crystal protein genes of *B. thuringiensis* or *B. sphaericus* (Table 17).

TABLE 17

***Bacillus* insecticidal crystal protein gene primers tested by PCR against AB78 DNA.**

Primers Tested	Product Produced
2 sets specific for CryIIIA	Negative
CryIIIB	Negative
2 sets specific for CryIA	Negative
CryIA(a)	Negative
CryIA(b) specific	Negative
CryIB	Negative
CryIC specific	Negative
CryIE specific	Negative
2 sets specific for <i>B. sphaericus</i>	Negative
2 sets specific for CryIV	Negative
<i>Bacillus</i> control (PI-PLC)	Positive

EXAMPLE 9. COSMID CLONING OF TOTAL DNA FROM *B. CEREUS* STRAIN

AB78

The VIP1A(a) gene was cloned from total DNA prepared from strain AB78 as follows:

Isolation of AB78 DNA was as follows:

1. Grow bacteria in 10 ml L-broth overnight. (Use 50 ml sterile centrifuge tube)
2. Add 25 ml of fresh L-broth and ampicillin (30 µg/ml).
3. Grow cells 2-6 h. at 30°C with shaking.
4. Spin cells in a 50 ml polypropylene orange cap tube in IEC benchtop clinical centrifuge at 3/4 speed.
5. Resuspend cell pellet in 10 ml TES (TES = 50 mM TRIS pH 8.0, 100 mM EDTA, 15 mM NaCl).
6. Add 30 mg lysozyme and incubate 2 hrs at 37°C.

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7. Add 200 μ l 20% SDS and 400 μ l Proteinase K stock (20 mg/ml). Incubate at 37°C.
8. Add 200 μ l fresh Proteinase K. Incubate 1 hr. at 55°C. Add 5 ml TES to make 15 ml final volume.
9. Phenol extract twice (10 ml phenol, spin at room temperature at 3/4 speed in an IEC benchtop clinical centrifuge). Transfer supernatant (upper phase) to a clean tube using a wide bore pipette.
10. Extract once with 1:1 vol. phenol:chloroform/isoamyl alcohol (24:1 ratio).
11. Precipitate DNA with an equal volume of cold isopropanol; Centrifuge to pellet DNA.
12. Resuspend pellet in 5 ml TE.
13. Precipitate DNA with 0.5 ml 3M NaOAc pH 5.2 and 11 ml 95% ethanol. Place at -20°C for 2 h.
14. "Hook" DNA from tube with a plastic loop, transfer to a microfuge tube, spin, pipette off excess ethanol, dry in vacuo.
15. Resuspend in 0.5 ml TE. Incubate 90 min. at 65°C to help get DNA back into solution.
16. Determine concentration using standard procedures.

Cosmid Cloning of AB78

All procedures, unless indicated otherwise, were performed according to Stratagene Protocol, Supercos 1 Instruction Manual, Cat. No. 251301.

Generally, the steps were as follows:

- A. Sau 3A partial digestion of the AB78 DNA.
- B. Preparation of vector DNA
- C. Ligation and packaging of DNA
- D. Titering the cosmid library
 1. Start a culture of HB101 cells by placing 50 ml of an overnight culture in 5 mls of TB with 0.2% maltose. Incubate 3.5 hrs. at 37°C.
 2. Spin out cells and resuspend in 0.5 ml 10 mM MgSO₄.
 3. Add together:
 - 100 μ l cells
 - 100 μ l diluted packaging mixture
 - 100 μ l 10 mM MgSO₄

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30 l TB

4. Adsorb at room temperature for 30 minutes with no shaking.
5. Add 1 ml TB and mix gently. Incubate 30 minutes at 37°C.
6. Plate 200 l onto L-amp plates. Incubate at 37°C overnight.

At least 400 cosmid clones were selected at random and screened for activity against western corn rootworm as described in Example 3. DNA from 5 active clones and 5 non-active clones were used in Southern hybridizations. Results demonstrated that hybridization using the above described oligonucleotide probe correlated with western corn rootworm activity (Table 18).

Cosmid clones P3-12 and P5-4 have been deposited with the Agricultural Research Service Patent Culture Collection (NRRL) and given Accession Nos. NRRL B-21061 and NRRL B-21059 respectively.

TABLE 18

Activity of AB78 cosmid clones against western corn rootworm.

Clone	Mean percent mortality (N=4)
-------	---------------------------------

Clones which hybridize with probe

P1-73	47
P1-83	64
P2-2	69
P3-12	85
P5-4	97

Clones which do not hybridize with probe

P1-2	5
P3-8	4

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P3-9	12
P3-18	0
P4-6	9

EXAMPLE 10. IDENTIFICATION OF A 6 KB REGION ACTIVE AGAINST WESTERN CORN ROOTWORM.

DNA from P3-12 was partially digested with restriction enzyme *Sau* 3A, and ligated into the *E. coli* vector pUC19 and transformed into *E. coli*. A DNA probe specific for the 80 kDa VIP1A(a) protein was synthesized by PCR amplification of a portion of P3-12 DNA. Oligonucleotides MK113 and MK117, which hybridize to portions of VIP1A(a), were synthesized using the partial amino acid sequence of the 80 kDa protein. Plasmid subclones were identified by colony hybridization to the PCR-generated probe, and tested for activity against western corn rootworm. One such clone, PL2, hybridized to the PCR-generated fragment, and was active against western corn rootworm in the assay previously described.

A 6 kb *Cla* I restriction fragment from pL2 was cloned into the *Sma* I site of the *E. coli*-*Bacillus* shuttle vector pHT 3101 (Lereclus, D. *et al.*, FEMS Microbiology Letters 60:211-218 (1989)) to yield pCIB6201. This construct confers anti-western corn rootworm activity upon both *Bacillus* and *E. coli* strains, in either orientation. pCIB6022 contains this same 6 kb *Cla* I fragment in pBluescript SK(+) (Stratagene), produces equivalent VIP1A(a) protein (by western blot), and is also active against western corn rootworm.

The nucleotide sequence of pCIB6022 was determined by the dideoxy termination method of Sanger *et al.*, Proc. Natl. Acad. Sci. USA, 74:5463-5467 (1977), using PRISM Ready Reaction Dye Deoxy Terminator Cycle Sequencing Kits and PRISM Sequenase® Terminator Double-Stranded DNA Sequencing Kit and analyzed on an ABI 373 automatic sequencer. The sequence is given in SEQ ID NO:1. The 6 kb fragment encodes both VIP1A(a) and VIP2A(a), as indicated by the open reading frames described in SEQ ID NO:1. The sequence encoding VIP2A(a) is further disclosed in SEQ ID NO:4. The relationship between VIP1A(a) and VIP2A(a) within the 6 kb fragment found in pCIB6022 is depicted in Table 19. pCIB6022 was

deposited with the Agricultural Research Service, Patent Culture Collection, (NRRL), Northern Regional Research Center, 1815 North University Street, Peoria, Illinois 61604, USA, and given the Accession No. NRRL B-21222.

EXAMPLE 11. FUNCTIONAL DISSECTION OF THE VIP1A(a) DNA REGION.

To confirm that the VIP1A(a) open reading frame (ORF) is necessary for insecticidal activity a translational frameshift mutation was created in the gene. The restriction enzyme Bgl II recognizes a unique site located 857 bp into the coding region of VIP1A(a). pCIB6201 was digested with Bgl II, and the single-stranded ends filled-in with DNA polymerase (Klenow fragment) and dNTPS. The plasmid was religated and transformed into *E. coli*. The resulting plasmid, pCIB6203, contains a four nucleotide insertion in the coding region of VIP1A(a). pCIB6203 does not confer WCRW insecticidal activity, confirming that VIP1A(a) is an essential component of western corn rootworm activity.

To further define the region necessary to encode VIP1A(a), subclones of the VIP1A(a) and VIP2A(a) (auxiliary protein) region were constructed and tested for their ability to complement the mutation in pCIB6203. pCIB6023 contains the 3.7kb Xba I-EcoRV fragment in pBluescript SK(+) (Stratagene). Western blot analysis indicates that pCIB6023 produces VIP1A(a) protein of equal size and quantity as clones PL2 and pCIB6022. pCIB6023 contains the entire gene encoding the 80 kD protein. pCIB6023 was deposited with the Agricultural Research Service, Patent Culture Collection, (NRRL), Northern Regional Research Center, 1815 North University Street, Peoria, Illinois 61604, USA, and given the Accession No. NRRL B-21223N. pCIB6206 contains the 4.3 kb Xba I-Cla I fragment from pCIB6022 in pBluescript SK(+) (Stratagene). pCIB6206 was also deposited with the Agricultural Research Service, Patent Culture Collection, (NRRL), Northern Regional Research Center, 1815 North University Street, Peoria, Illinois 61604, USA, and given the Accession No. NRRL B-21321.

pCIB6023, pCIB6206, and pCIB6203 do not produce detectable western corn rootworm activity when tested individually. However, a mixture of cells containing pCIB6203 (VIP1A(a)-mutated, plus VIP2A(a)) and cells containing pCIB6023 (only

VIP1A(a)) shows high activity against western corn rootworm. Similarly, a mixture of cells containing pCIB6206 and cells containing pCIB6203 shows high activity against western corn rootworm.

To further define the limits of VIP2A(a), we constructed pCIB6024, which contains the entirety of VIP2A(a), but lacks most of the VIP1A(a) coding region. pCIB6024 was constructed by gel purifying the 2.2 kb Cla I-Sca I restriction fragment from pCIB6022, filling in the single-stranded ends with DNA polymerase (Klenow fragment) and dNTPs, and ligating this fragment into pBluescript SK(+) vector (Stratagene) digested with the enzyme Eco RV. Cells containing pCIB6024 exhibit no activity against western corn rootworm. However, a mixture of cells containing pCIB6024 and cells containing pCIB6023 shows high activity against western corn rootworm. (See Table 19).

Thus, pCIB6023 and pCIB6206 must produce a functional VIP1A(a) gene product, while pCIB6203 and pCIB6024 must produce a functional VIP2A(a) gene product. These results suggest a requirement for a gene product(s) from the VIP2A(a) region, in combination with VIP1A(a), to confer maximal western corn rootworm activity. (See Table 19.)

Table 19
Characterization of pCIB6022

		Activity vs. WCRW
	pCIB6022	+++
	pCIB6023	—
	pCIB6023	—
	pCIB6026	—
	pCIB6024	—

Functional Complementation of VIP

	pCIB6023	+++
	pCIB6023	+++
	pCIB6023	+++
	pCIB6026	+++
	pCIB6023	+++
	pCIB6024	+++

Boxed regions represent the extent of VIP1A(a) and VIP2A(a). White box represents the portion of VIP1 encoding the 80 kDa peptide observed in *Bacillus*. Dark box represents the N-terminal 'propeptide' of VIP1A(a) predicted by DNA sequence analysis. Stippled box represents the VIP2A(a) coding region. Large 'X' represents the location of the frameshift mutation introduced into VIP1A(a). Arrows represent constructs transcribed by the beta-galactosidase

EXAMPLE 12. AB78 ANTIBODY PRODUCTION

Antibody production was initiated in 2 Lewis rats to allow for both the possibility of moving to production of hybridoma cell lines and also to produce enough serum for limited screening of genomic DNA library. Another factor was the very limited amount of antigen available and the fact that it could only be produced to purity by PAGE and subsequent electrotransfer to nitrocellulose.

Due to the limited availability of antigen on nitrocellulose, the nitrocellulose was emulsified in DMSO and injected into the hind footpads of the animals to elicit B-cell production in the popliteal lymph nodes just upstream. A strong reacting serum was produced as judged by western blot analysis with the first production bleed. Several subsequent injections and bleeds produced enough serum to accomplish all of the screening required.

Hybridoma production with one of the rats was then initiated. The popliteal lymph node was excised, macerated, and the resulting cells fused with mouse myeloma P3x63Ag8.653. Subsequent cell screening was accomplished as described below. Four initial wells were selected which gave the highest emulsified antigen reaction to be moved to limited dilution cloning. An additional 10 wells were chosen for expansion and cryopreservation.

Procedure to Emulsify AB78 on nitrocellulose in DMSO for ELISA screening:

After electrotransfer of AB78 samples run on PAGE to nitrocellulose, the reversible strain Ponceau S is used to visualize all protein transferred. The band corresponding to AB78 toxin, previously identified and N-terminal sequenced, was identified and excised from nitrocellulose. Each band is approximately 1 mm x 5 mm in size to minimize the amount of nitrocellulose emulsified. A single band is placed in a microfuge tube with 250 µl of DMSO and macerated using a plastic pestle (Kontes, Vineland, NJ). To aid in emulsification, the DMSO mixture is heated for 2-3 minutes at 37 C-45 C. Some further maceration might be necessary following heating; however, all of the nitrocellulose should be emulsified. Once the AB78 sample is emulsified, it is placed on ice. In preparation for microtiter plate coating with the emulsified antigen, the sample must be diluted in borate buffered saline as follows: 1:5, 1:10, 1:15, 1:20, 1:30, 1:50, 1:100, and 0. The coating antigen must be prepared fresh immediately prior to use.

ELISA protocol:

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1. Coat with AB78/DMSO in BBS. Incubate overnight at 4°C.
2. Wash plate 3X with 1X ELISA wash buffer.
3. Block (1% BSA & 0.05% Tween 20 in PBS) for 30 minutes at Room Temperature.
4. Wash plate 3X with 1X ELISA wash buffer.
5. Add rat serum. Incubate 1.5 hours at 37°C.
6. Wash plate 3X with 1X ELISA wash buffer.
7. Add goat anti-rat at a concentration of 2 µg/ml in ELISA diluent. Incubate 1 hr. at 37°C.
8. Wash plate 3X with 1X ELISA wash buffer.
9. Add rabbit anti-goat alkaline phosphatase at 2 µg/ml in ELISA diluent. Incubate 1 hr. at 37°C.
10. Wash 3X with 1X ELISA wash buffer.
11. Add Substrate. Incubate 30 minutes at room temperature.
12. Stop with 3N NaOH after 30 minutes.

Preparation of VIP2A(a) Antisera

A partially purified AB78 culture supernatant was separated by discontinuous SDS PAGE (Novex) following manufacturer's instructions. Separated proteins were electrophoresed to nitrocellulose (S&S #21640) as described by Towbin *et al.*, (1979). The nitrocellulose was stained with Ponceau S and the VIP2A(a) band identified. The VIP2A(a) band was excised and emulsified in DMSO immediately prior to injection. A rabbit was initially immunized with emulsified VIP2A(a) mixed approximately 1:1 with Freund's Complete adjuvant by intramuscular injection at four different sites. Subsequent immunizations occurred at four week intervals and were identical to the first, except for the use of Freund' Incomplete adjuvant. The first serum harvested following immunization reacted with VIP2A(a) protein. Western blot analysis of AB78 culture supernatant using this antisera identifies predominately full length VIP2A(a) protein.

EXAMPLE 13. ACTIVATION OF INSECTICIDAL ACTIVITY OF NON-ACTIVE BT STRAINS WITH AB78 VIP CLONES.

Adding pCIB6203 together with a 24 h culture (early to mid-log phase) supernatant from Bt strain GC91 produces 100% mortality in *Diabrotica virgifera virgifera*. Neither pCIB6203 nor GC91 is active on *Diabrotica virgifera virgifera* by itself. Data are shown below:

Test material	Percent <i>Diabrotica</i> mortality
pCIB6203	0
GC91	16
pCIB6203 + GC91	100
Control	0

EXAMPLE 14. ISOLATION AND BIOLOGICAL ACTIVITY OF *B. CEREUS* AB81.

A second *B. cereus* strain, designated AB81, was isolated from grain bin dust samples by standard methodologies. A subculture of AB81 was grown and prepared for bioassay as described in Example 2. Biological activity was evaluated as described in Example 3. The results are as follows:

Insect species tested	Percent Mortality
<i>Ostrinia nubilalis</i>	0
<i>Agrotis ipsilon</i>	0
<i>Diabrotica virgifera virgifera</i>	55

EXAMPLE 15. ISOLATION AND BIOLOGICAL ACTIVITY OF**B. THURINGIENSIS AB6.**

A *B. thuringiensis* strain, designated AB6, was isolated from grain bin dust samples by standard methods known in the art. A subculture of AB6 was grown and prepared for bioassay as described in Example 2. Half of the sample was autoclaved 15 minutes to test for the presence of β -exotoxin.

Biological activity was evaluated as described in Example 3. The results are as follows:

<u>Insect species</u>	<u>Percent</u>
<u>tested</u>	<u>Mortality</u>
<i>Ostrinia nubilalis</i>	0
<i>Agrotis ipsilon</i>	100
<i>Agrotis ipsilon</i> (autoclaved sample)	0
<i>Diabrotica virgifera virgifera</i>	0

The reduction of insecticidal activity of the culture supernatant to insignificant levels by autoclaving indicates that the active principle is not β -exotoxin.

Strain AB6 has been deposited in the Agricultural Research Service, Patent Culture Collection (NRRL), Northern Regional Research Center, 1815 North University Street, Peoria, Illinois 61604, USA, and given Accession No. NRRL B-21060.

EXAMPLE 16. ISOLATION AND BIOLOGICAL CHARACTERIZATION OF**B. THURINGIENSIS AB88.**

A Bt strain, designated AB88, was isolated from grain bin dust samples by standard methodologies. A subculture of AB88 was grown and prepared for bioassay as described in Example 2. Half of the sample was autoclaved 15 minutes to test for the presence of β -exotoxin. Biological activity was evaluated against a number of insect species as described in Example 3. The results are as follows:

Insect species tested	Order	Percent mortality of culture supernatant	
		Non-autoclaved	Autoclaved
<i>Agrotis ipsilon</i>	<i>Lepidoptera</i>	100	5
<i>Ostrinia nubilalis</i>	<i>Lepidoptera</i>	100	0
<i>Spodoptera frugiperda</i>	<i>Lepidoptera</i>	100	4
<i>Helicoverpa zea</i>	<i>Lepidoptera</i>	100	12
<i>Heliothis virescens</i>	<i>Lepidoptera</i>	100	12
<i>Leptinotarsa decemlineata</i>	<i>Coleoptera</i>	0	0
<i>Diabrotica virgifera</i>	<i>Coleoptera</i>	0	5
<i>virgifera</i>			

The reduction of insecticidal activity of the culture supernatant to insignificant levels by autoclaving indicates that the active principle is not β -exotoxin.

Delta-endotoxin crystals were purified from strain AB88 by standard methodologies. No activity from pure crystals was observed when bioassayed against *Agrotis ipsilon*.

EXAMPLE 17. PURIFICATION OF VIPS FROM STRAIN AB88:

Bacterial liquid culture was grown overnight [for 12h] at 30°C in TB media. Cells were centrifuged at 5000 x g for 20 minutes and the supernatant retained. Proteins present in the supernatant were precipitated with ammonium sulfate (70% saturation),

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centrifuged [at 5000 x g for 15 minutes] and the pellet retained. The pellet was resuspended in the original volume of 20 mM Tris pH 7.5 and dialyzed overnight against the same buffer at 4°C. AB88 dialysate was more turbid than comparable material from AB78. The dialysate was titrated to pH 4.5 using 20 mM sodium citrate (pH 2.5) and, after 30 min incubation at room temperature, the solution was centrifuged at 3000 x g for 10 min. The protein pellet was redissolved in 20 mM Bis-Tris-Propane pH 9.0.

AB88 proteins have been separated by several different methods following clarification including isoelectric focusing (Rotofor, BioRad, Hercules, CA), precipitation at pH 4.5, ion-exchange chromatography, size exclusion chromatography and ultrafiltration.

Proteins were separated on a Poros HQ/N anion exchange column (PerSeptive Biosystems, Cambridge, MA) using a linear gradient from 0 to 500 mM NaCl in 20 mM Bis-Tris-Propane pH 9.0 at a flow rate of 4 ml/min. The insecticidal protein eluted at 250 mM NaCl.

European corn borer (ECB)-active protein remained in the pellet obtained by pH 4.5 precipitation of dialysate. When preparative IEF was done on the dialysate using pH 3-10 ampholytes, ECB insecticidal activity was found in all fractions with pH of 7 or greater. SDS-PAGE analysis of these fractions showed protein bands of MW ~60 kDa and ~80 kDa. The 60 kDa and 80 kDa bands were separated by anion exchange HPLC on a Poros-Q column (PerSeptive Biosystems, Cambridge, MA). N-terminal sequence was obtained from two fractions containing proteins of slightly differing MW, but both of approximately 60 kDa in size. The sequences obtained were similar to each other and to some δ -endotoxins.

anion exchange fraction 23 (smaller): xEPFVSAxxxQxxx (SEQ ID NO:10)

anion exchange fraction 28 (larger): xEYENVEPFVSAx (SEQ ID NO:11)

When the ECB-active pH 4.5 pellet was further separated by anion exchange on a Poros-Q column, activity was found only in fractions containing a major band of ~60 kDa.

Black cutworm-active protein also remained in the pellet when AB88 dialysate was brought down to pH 4.5. In preparative IEF using pH 3-10 ampholytes, activity was not found in the ECB-active IEF fractions; instead, it was highest in a fraction of pH 4.5-5.0. Its major components have molecular weights of ~35 and ~80 kDa.

The pH 4.5 pellet was separated by anion exchange HPLC to yield fractions containing only the 35 kDa material and fractions containing both 35 kDa and 80 kDa bands.

EXAMPLE 18. CHARACTERIZATION OF AB88 VIP.

Fractions containing the various lepidopteran active vegetative proteins were generated as described in Example 17. Fractions with insecticidal activity were separated in 8 to 16% SDS-polyacrylamide gels and transferred to PVDF membranes [LeGendre et al, (1989) in: A Practical Guide to Protein and Peptide Purification for Microsequencing, ed Matsudaria PT (Academic Press Inc, New York)]. Biological analysis of fractions demonstrated that different VIPs were responsible for the different lepidopteran species activity.

The *Agrotis ipsilon* activity is due to an 80 kDa and/or a 35 kDa protein, either delivered singly or in combination. These proteins are not related to any δ -endotoxins from Bt as evidenced by the lack of sequence homology of known Bt δ -endotoxin sequences. The vip3A(a) insecticidal protein from strain AB88 is present mostly (at least 75% of the total) in supernatants of AB88 cultures.

Also, these proteins are not found in the AB88 δ -endotoxin crystal. N-terminal sequences of the major δ -endotoxin proteins were compared with the N-terminal sequences of the 80 kDa and 35 kDa VIP and revealed no sequence homology. The N-terminal sequence of the vip3A(a) insecticidal protein possesses a number of positively charged residues (from Asn2 to Asn7) followed by a hydrophobic core region (from Thr8 to Ile34). Unlike most of the known secretion proteins, the vip3A(a) insecticidal protein from strain AB88 is not N-terminally processed during export.

A summary of the results follows:

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<i>Agrotis</i> VIP N-terminal sequences	N-terminal sequence of major δ -endotoxin proteins
	130 kDa MDNNPNINE (SEQ ID NO:14)
80 kDa MNKNNTKLPTRALP (SEQ ID NO:12)	80 kDa MDNNPNINE (SEQ ID NO:15)
	60 kDa MNVLNSGRTTI (SEQ ID NO:16)
35 kDa ALSENTGKDGGYIVP (SEQ ID NO:13)	

The *Ostrinia nubilalis* activity is due to a 60 kDa VIP and the *Spodoptera frugiperda* activity is due to a VIP of unknown size.

Bacillus thuringiensis strain AB88 has been deposited in the Agricultural Research Service, Patent Culture Collection (NRRL), Northern Regional Research Center, 1815 North University Street, Peoria, Illinois 61604, USA and given the Accession No. NRRL B-21225.

EXAMPLE 18A. ISOLATION AND BIOLOGICAL ACTIVITY OF *B. THURINGIENSIS* AB424

A *B. thuringiensis* strain, designated AB424, was isolated from a moss covered pine cone sample by standard methods known in the art. A subculture of AB424 was grown and prepared for bioassay as described in Example 2.

Biological activity was evaluated as described in Example 3. The results are as follows:

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Insect species tested	Percent mortality
<i>Ostrinia nubilalis</i>	100
<i>Agrotis ipsilon</i>	100
<i>Diabrotica virgifera</i> <i>virgifera</i>	0

Strain AB424 has been deposited in the Agricultural Research Service, Patent Culture Collection (NRRL), Northern Regional Research Center, 1815 North University Street, Peoria, Illinois 61604, USA, and given Accession No. NRRL B-21439.

EXAMPLE 18B. CLONING OF THE VIP3A(a) and VIP3A(b) GENES WHICH ENCODE PROTEINS ACTIVE AGAINST BLACK CUTWORM.

Total DNA from isolates AB88 and AB424 was isolated [Ausubel et al (1988), in: Current Protocols in Molecular Biology (John Wiley & Sons, NY)] and digested with the restriction enzymes *Xba*I [library of 4.0 to 5.0 Kb size-fractionated *Xba*I fragments of *B thuringiensis* AB88 DNA] and *Eco*RI [library of 4.5 to 6.0 Kb size-fractionated *Eco*RI fragments *B thuringiensis* AB424 DNA] respectively, ligated into pBluescript vector previously linearized with the same enzymes and dephosphorylated, and transformed into *E. coli* DH5 α strain. Recombinant clones were blotted onto nitrocellulose filters which were subsequently probed with a ³²P labeled 33-bases long oligonucleotide corresponding to the 11-N terminal amino acids of the 80 kDa protein active against *Agrotis ipsilon* (black cutworm). Hybridization was carried out at 42°C in 2 x SSC/0.1% SDS (1 x SSC = 0.15 M NaCl/0.015 M sodium citrate, pH 7.4) for 5 min and twice at 50°C in 1 x SSC/0.1 SDS for 10 min. Four out of 400 recombinant clones were positive. Insect bioassays of the positive recombinants exhibited toxicity to black cutworm larvae comparable to that of AB88 or AB424 supernatants.

Plasmid pCIB7104 contains a 4.5 Kb *XbaI* fragment of AB88 DNA. Subclones were constructed to define the coding region of the insecticidal protein.

E coli pCIB7105 was constructed by cloning the 3.5 Kb *XbaI*-*AccI* fragment of pCIB7104 into pBluescript.

Plasmid pCIB7106 contained a 5.0 Kb *EcoRI* fragment of AB424 DNA. This fragment was further digested with *HincII* to render a 2.8 kb *EcoRI*-*HincII* insert (pCIB7107), which still encoded a functional insecticidal protein.

The nucleotide sequence of pCIB7104, a positive recombinant clone from AB88, and of pCIB7107, a positive recombinant clone from AB424, was determined by the dideoxy termination method of Sanger *et al.*, Proc. Natl. Acad. Sci. USA, 74: 5463-5467 (1977), using PRISM Ready Reaction Dye Deoxy Terminator Cycle Sequencing Kits and PRISM Sequenase® Terminator Double-Stranded DNA Sequencing Kit and analysed on an ABI 373 automatic sequencer.

The clone pCIB7104 contains the VIP3A(a) gene whose coding region is disclosed in SEQ ID NO:28 and the encoded protein sequence is disclosed in SEQ ID NO:29. A synthetic version of the coding region designed to be highly expressed in maize is given in SEQ ID NO:30. Any number of synthetic genes can be designed based on the amino acid sequence given in SEQ ID NO:29.

The clone pCIB7107 contains the VIP3A(b) gene whose coding region is disclosed in SEQ ID NO:31 and the encoded protein is disclosed in SEQ ID NO:32. Both pCIB7104 and pCIB7107 have been deposited with the Agricultural Research Service Patent Culture Collection (NRRL) and given Accession Nos. NRRL B-21422 and B-21423, respectively.

The VIP3A(a) gene contains an open reading frame (ORF) that extends from nucleotide 732 to 3105. This ORF encodes a peptide of 791 amino acids corresponding to a molecular mass of 88,500 daltons. A Shine-Dalgarno (SD) sequence is located 6 bases before the first methionine and its sequence identifies a strong SD for *Bacillus*.

The VIP3A(b) gene is 98% identical to VIP3A(a).

When blot of total DNA isolated from AB88 *B. thuringiensis* cells were probed with a 33-base fragment that spans the N-terminal region of the VIP3A-insecticidal protein, single bands could be observed in different restriction digests. This result was

confirmed by using larger probes spanning the coding region of the gene. A search of the GenBank data base revealed no homology to known proteins.

EXAMPLE 18C. EXPRESSION OF THE VIP3A INSECTICIDAL PROTEINS

The time course for expression of the VIP3A(a) insecticidal protein was analyzed by western blot. Samples from *Bacillus thuringiensis* Ab88 cultures were taken throughout its growth curve and sporulation. The VIP3A(a) insecticidal protein can be detected in the supernatants of AB88 cultures during logarithmic phase, as early as 15 h after initiating the culture. It reached its maximum level during early stages of stationary phase and remained at high levels during and after sporulation. Similar results were obtained when supernatants of AB424 *Bacillus cereus* cultures were used. The levels of VIP3A(a) insecticidal protein reflected the expression of the VIP3A(a) gene as determined by Northern blot. The initiation of the sporulation was determined by direct microscopic observations and by analyzing the presence of δ -endotoxins in cell pellets. Cry-I type proteins could be detected late in the stationary phase, during and after sporulation.

EXAMPLE 18D. IDENTIFICATION OF NOVEL VIP3-LIKE GENES BY HYBRIDIZATION

To identify *Bacillus* containing genes related to the VIP3A(a) from isolate AB88, a collection of *Bacillus* isolates was screened by hybridization. Cultures of 463 *Bacillus* strains were grown in microtiter wells until sporulation. A 96-pin colony stampel was used to transfer the cultures to 150 mm plates containing L-agar. Inoculated plates were kept at 30°C for 10 hours, then at 4°C overnight. Colonies were blotted onto nylon filters and probed with a 1.2Kb *Hind*III VIP3A(a) derived fragment. Hybridization was performed overnight at 62°C using hybridization conditions of Maniatis *et al.* Molecular Cloning: A Laboratory Manual (1982). Filters were washed with 2xSSC/0.1% SDS at 62°C and exposed to X-ray film.

Of the 463 *Bacillus* strains screened, 60 contain VIP3-like genes that could be detected by hybridization. Further characterization of some of them (AB6 and AB426)

showed that their supernatants contain a BCW insecticidal protein similar to the Vip3 protein that are active against black cutworm.

EXAMPLE 18E. CHARACTERIZATION OF A *B. thuringiensis* STRAIN M2194 CONTAINING A CRYPTIC VIP3-LIKE GENE

A *B. thuringiensis* strain, designated M2194, was shown to contain VIP3-like gene(s) by colony hybridization as described in Example 18C. The M2194 VIP3 like gene is considered cryptic since no expression can be detected throughout the bacterial growth phases either by immunoblot analysis using polyclonal antibodies raised against the VIP3A(a) protein isolated from AB88 or by bioassay as described in Example 3.

Antiserum against purified VIP3A(a) insecticidal protein was produced in rabbits. Nitrocellulose-bound protein (50 µg) was dissolved in DMSO and emulsified with Freund's complete adjuvant (Difco). Two rabbits were given subcutaneous injections each month for three month. They were bled 10 days after the second and third injection and the serum was recovered from the blood sample [Harlow et al (1988) in : Antibodies: A Laboratory Manual (Cold Spring Harbor Lab Press, Plainview, NY)].

The M2194 VIP3-like gene was cloned into pKS by following the protocol described in Example 9, which created pCIB7108. *E. coli* containing pCIB7108 which comprises the M2194 VIP3 gene were active against black cutworm demonstrating that the gene encodes a functional protein with insecticidal activity. The plasmid pCIB7108 has been deposited with the Agricultural Research Service Patent Culture Collection (NRRL) and given Accession No. NRRL B-21438.

EXAMPLE 18F. INSECTICIDAL ACTIVITY OF VIP3A PROTEINS

The activity spectrum of VIP3A insecticidal proteins was qualitatively determined in insect bioassays in which recombinant *E coli* carrying the VIP³A genes were fed to larvae. In these assays, cells carrying the VIP3A(a) and VIP3A(b) genes were insecticidal to *Agrotis ipsilon*, *Spodoptera frugiperda*, *Spodoptera exigua*, *Heliothis virescens* and *Helicoverpa zea*. Under the same experimental conditions, bacterial extracts containing VIP3A proteins did not show any activity against *Ostrinia nubilalis*.

Effect of VIP⁺A insecticidal proteins on *Agrotis ipsilon* larvae

Treatment	(%) Mortality
TB medium	5
AB88 Supernatant	100
Ab424 Supernatant	100
Buffer	7
<i>E coli</i> pKS	10
<i>E coli</i> pCIB7104 (AB88)	100
<i>E coli</i> pCIB7105 (AB88)	100
<i>E coli</i> pCIB7106 (AB424)	100
<i>E coli</i> pCIB7107 (AB424)	100

Effect of VIP3A insecticidal proteins on lepidopteran insect larvae

Treatment	Insect	(%) Mortality
<i>E coli</i> pKS	BCW	10
	FAW	5
	BAW	10
	TBW	8
	CEW	10
	ECB	5
<i>E coli</i> pCIB7105		
<i>E coli</i> pCIB7107	BCW	100
	FAW	100
	BAW	100
	TBW	100
	CEW	50
	ECB	10

BCW = Black Cut Worm; FAW = Fall Army Worm; BAW = Beet Army Worm; TBW = Tobacco Bud Worm; CEW = Corn Ear Worm; ECB = European Corn Borer

**EXAMPLE 19. ISOLATION AND BIOLOGICAL ACTIVITY OF OTHER
BACILLUS SP.**

Other *Bacillus* species have been isolated which produce proteins with insecticidal activity during vegetative growth. These strains were isolated from environmental samples by standard methodologies. Isolates were prepared for bioassay and assayed as described in Examples 2 and 3 respectively. Isolates which produced insecticidal proteins during vegetative growth with activity against *Agrotis ipsilon* in the bioassay are tabulated below. No correlation was observed between the presence of a δ -endotoxin crystal and vegetative insecticidal protein production.

<i>Bacillus</i> isolate	Presence of δ - endotoxin crystal	Percent mortality
AB6	+	100
AB53	-	80
AB88	+	100
AB195	-	60
AB211	-	70
AB217	-	83
AB272	-	80
AB279	-	70
AB289	+	100
AB292	+	80
AB294	-	100
AB300	-	80
AB359	-	100

Isolates AB289, AB294 and AB359 have been deposited in the Agricultural Research Service, Patent Culture Collection (NRRL), Northern Regional Research Center, 1815 North University Street, Peoria IL 61604, USA and given the Accession Numbers NRRL B-21227, NRRL B-21229, and NRRL B-21226 respectively.

Bacillus isolates which produce insecticidal proteins during vegetative growth with activity against *Diabrotica virgifera virgifera* are tabulated below.

<i>Bacillus</i> isolate	Presence of δ - endotoxin crystal	Percent mortality
AB52	-	50
AB59	-	71
AB68	+	60
AB78	-	100
AB122	-	57
AB218	-	64
AB256	-	64

Isolates AB59 and AB256 have been deposited in the Agricultural Research Service, Patent Culture Collection (NRRL), Northern Regional Research Center, 1815 North University Street, Peoria Illinois 61604, USA, and given the Accession Numbers NRRL B-21228 and NRRL B-21230, respectively.

EXAMPLE 20. IDENTIFICATION OF NOVEL VIP1/VIP2 LIKE GENES BY HYBRIDIZATION

To identify strains containing genes related to those found in the VIP1A(a)/VIP2A(a) region of AB78, a collection of *Bacillus* strains was screened by hybridization. Independent cultures of 463 *Bacillus* strains were grown in wells of 96 well microtiter dishes (five plates total) until the cultures sporulated. Of the strains tested, 288 were categorized as *Bacillus thuringiensis*, and 175 were categorized as other *Bacillus* species based on the presence or absence of δ -endotoxin crystals. For each microtiter dish, a 96-pin colony stamper was used to transfer approximately 10 μ l of spore culture to two 150 mm plates containing L-agar. Inoculated plates were grown 4-8 hours at 30 °C, then chilled to 4 °C. Colonies were transferred to nylon filters, and the cells lysed by standard methods known in the art. The filters were hybridized to a DNA probe generated from DNA fragments containing both VIP1A(a) and VIP2A(a) DNA sequences. Hybridization was performed overnight at 65 °C using the hybridization conditions of Church and Gilbert (Church, G.M., and W. Gilbert,

PNAS, 81:1991-1995 (1984)). Filters were washed with 2x SSC containing 0.1% SDS at 65 °C and exposed to X-Ray film.

Of the 463 *Bacillus* strains screened, 55 strains were identified that hybridized to the VIP1A(a)/VIP2A(a) probe. DNA was isolated from 22 of these strains, and analyzed using a Southern blot with VIP1A(a)/VIP2A(a) DNA as probes. These strains were grouped into 8 classes based on their Southern blot pattern. Each class differed in Southern blot pattern from AB78. One class had a pattern identical to that of the VIP1A(a)/VIP2A(a) homologs from *Bacillus thuringiensis* var *tenebrionis* (see below). Each of the 22 strains was tested for activity against western corn rootworm (WCRW). Three strains, AB433, AB434, and AB435 were found to be active on WCRW. Western blot analysis using VIP2A(a) antisera revealed that strains AB6, AB433, AB434, AB435, AB444, and AB445 produce a protein(s) of equivalent size to VIP2A(a).

Notable among the strains identified was *Bacillus thuringiensis* strain AB6, (NRRL B-21060) which produced a VIP active against black cutworm (*Agrotis ipsilon*) as described in Example 15. Western blot analysis with polyclonal antisera to VIP2A(a) and polyclonal antisera to VIP1A(a) suggests that AB6 produces proteins similar to VIP2A(a) and VIP1A(a). Thus, AB6 may contain VIPs similar to VIP1A(a) and VIP2A(a), but with a different spectrum of insecticidal activity.

EXAMPLE 21. CLONING OF A VIP1A(a)/VIP2A(a) HOMOLOG FROM BACILLUS THURINGIENSIS VAR. TENEBRIONIS.

Several previously characterized *Bacillus* strains were tested for presence of DNA similar to VIP1A(a)/VIP2A(a) by Southern blot analysis. DNA from *Bacillus* strains AB78, AB88, GC91, HD-1 and ATCC 10876 was analyzed for presence of VIP1A(a)/VIP2A(a) like sequences. DNA from Bt strains GC91 and HD-1, and the Bc strain ATCC 10876 did not hybridize to VIP2A(a)/VIP1A(a) DNA, indicating they lack DNA sequences similar to VIP1A(a)/VIP2A(a) genes. Similarly, DNA from the insecticidal strain AB88 (Example 16) did not hybridize to VIP1A(a)/VIP2A(a) DNA region, suggesting that the VIP activity produced by this strain does not result from VIP1A(a)/VIP2A(a) homologs. In contrast, *Bacillus thuringiensis* var. *tenebrionis* (Btt)

contained sequences that hybridized to the VIP1A(a)/VIP2A(a) region. Further analysis confirmed that Btt contains VIP1A(a)/VIP2A(a) like sequences.

To characterize the Btt homologs of VIP2A(a) and VIP1A(a), the genes encoding these proteins were cloned. Southern blot analysis identified a 9.5 kb Eco RI restriction fragment likely to contain the coding regions for the homologs. Genomic DNA was digested with Eco RI, and DNA fragments of approximately 9.5 kb in length were gel-purified. This DNA was ligated into pBluescript SK(+) digested with Eco RI, and transformed into *E. coli* to generate a plasmid library. Approximately 10,000 colonies were screened by colony hybridization for the presence of VIP2A(a) homologous sequences. Twenty eight positive colonies were identified. All twenty eight clones are identical, and contain VIP1A(a)/VIP2A(a) homologs. Clone pCIB7100 has been deposited in the Agricultural Research Service, Patent Culture Collection (NRRL), Northern Regional Research Center, 1815 North University Street, Peoria Illinois 61604, USA, and given the Accession Number B-21322. Several subclones were constructed from pCIB7100. A 3.8 kb Xba I fragment from pCIB7100 was cloned into pBluescript SK(+) to yield pCIB7101. A 1.8 kb Hind III fragment and a 1.4 kb Hind III fragment from pCIB7100 were cloned into pBluescript SK(+) to yield pCIB7102 and pCIB7103, respectively. Subclones pCIB7101, pCIB7102 and pCIB7103 have been deposited in the Agricultural Research Service, Patent Culture Collection (NRRL), Northern Regional Research Center, 1815 North University Street, Peoria Illinois 61604, USA, and given the Accession Numbers B-21323, B-21324 and B-21325 respectively.

The DNA sequence of the region of pCIB7100 containing the VIP2A(a)/VIP1A(a) homologs was determined by the dideoxy chain termination method (Sanger *et al.*, 1977, Proc. Natl. Acad. Sci. USA 74:5463-5467). Reactions were performed using PRISM Ready Reaction Dye Deoxy Terminator Cycle Sequencing Kits and PRISM Sequenase® Terminator Double-Stranded DNA Sequencing Kits, and analyzed on an ABI model 373 automated sequencer. Custom oligonucleotides were used as primers to determine the DNA sequence in certain regions. The DNA sequence of this region is shown in SEQ ID NO:19.

The 4 kb region shown in SEQ ID NO:19 contains two open readings frames (ORFs), which encode proteins with a high degree of similarity to VIP1A(a) and VIP2A(a) proteins from strain AB78. The amino acid sequence of the VIP2A(a)

homolog, designated as VIP2A(b) using the standardized nomenclature, is found at SEQ ID NO:20 and the amino acid sequence of the VIP1A(a) homolog, designated as VIP1A(b) using the standardized nomenclature, is disclosed at SEQ ID NO:21. The VIP2A(b) protein exhibits 91% amino acid identity to VIP2A(a) from AB78. An alignment of the amino acid sequences of the two VIP2 proteins is provided in Table 20. The VIP1A(b) protein exhibits 77 % amino acid identity to VIP1A(a) from AB78. An alignment of these two VIP1 proteins is provided in Table 21. The alignment shown in Table 21 discloses the similarity between VIP1A(b) and VIP1A(a) from AB78. This alignment reveals that the amino terminal regions of the two VIP1 proteins share higher amino acid identity in the amino-terminal region than in the carboxy terminal region. In fact, the amino terminal two thirds (up to aa 618 of the VIP1A(b) sequence shown in Table 21) of the two proteins exhibit 91% identity, while the carboxy-terminal third (from aa 619-833 of VIP1A(b)) exhibit only 35% identity.

Western blot analysis indicated that *Bacillus thuringiensis* var. *tenebrionis* (Btt) produces both VIP1A(a) like and VIP2A(a) like proteins. However, these proteins do not appear to have activity against western corn rootworm. Bioassay for activity against western corn rootworm was performed using either a 24 h culture supernatant from Btt or *E. coli* clone pCIB7100 (which contains the entire region of the VIP1A(a)/VIP2A(a) homologs). No activity against western corn rootworm was detected in either case.

Given the similarity between the VIP2 proteins from Btt and AB78, the ability of VIP2A(b) from Btt to substitute for VIP2A(a) from AB78 was tested. Cells containing pCIB6206 (which produces AB78 VIP1A(a) but not VIP2A(a) protein) were mixed with Btt culture supernatant, and tested for activity against western corn rootworm. While neither Btt culture supernatant nor cells containing pCIB6206 had activity on WCRW, the mixture of Btt and pCIB6206 gave high activity against WCRW. Furthermore, additional bioassay showed that the Btt clone pCIB7100, which contains the Btt VIP1A(b)/VIP2A(b) genes in *E. coli*, also confers activity against WCRW when mixed with pCIB6206. Thus, the VIP2A(b) protein produced by Btt is functionally equivalent to the VIP2A(a) protein produced by AB78.

Thus, the ability to identify new strains with insecticidal activity by using VIP DNA as hybridization probes has been demonstrated. Furthermore, *Bacillus* strains that contain VIP1A(a)/VIP2A(a) like sequences, produce VIP1A(a)/VIP2A(a) like protein.

yet demonstrate toxicity toward different insect pests. Similar methods can identify many more members of the VIP1/VIP2 family. Furthermore, use of similar methods can identify homologs of other varieties of VIPs (for example, the VIPs from AB88).

TABLE 20

Alignment of VIP2 Amino Acid Sequences from *Bacillus thuringiensis* var. *tenebrionis* (VIP2A(b)) vs. AB78 (VIP2A(a))

```

Btt      1 MQRMEGKLFVVSKTQVWTRTVLLSTVYSITLLNNVVIKADQLNINSQSK 50 SEQ ID NO:20
          |.|||||:|.|.||||:|||||:|.||| |||:|||||||
AB78     1 MKRMEGKLFMVSKKLQVVTKTVLLSTVFSISLLNNEVIKAEQLNINSQSK 50 SEQ ID NO:2

51 YTNLQNLKIPDNAEDFKEDKGKAKEWGKEKGEWRPPATEKGEMNFLDN 100
          |||||.|..|||||:|||||||:|.||: .|||.|||||
51 YTNLQNLKITDKVEDFKEDKEKAKEWGKEKEKEWKL TATEKGKMNFLDN 100

101 KNDIKTNYKEITFSMAGSCEDIKDL EEIDKIFDKANLSSSIITYKNVEP 150
          ||| ||||| ||||| |||||.|||:|.|.||| |||||
101 KNDIXTNYKEITFSMAGSFEDIKDLKEIDKMF DKTNLSNSIITYKNVEP 150

151 ATIGFNKSLTEGNTINSDAMAQFKEQFLGKDMKFDSYLDTHLTAQQVSSK 200
          .||||| ||||| ||||| ||||| |||||:|:| ||||| |||||
151 TTIGFNKSLTEGNTINSDAMAQFKEQFLDRDIKFDSYLDTHLTAQQVSSK 200

201 KRVILKVTVP SGKGSTTP TKAGVILNNNEYKMLIDNGYVLHVDKVSQVVK 250
          .||||| ||||| ||||| ||||| |||||.|||||:|:| |||||
201 ERVILKVTVP SGKGSTTP TKAGVILNNSEYKMLIDNGYMHVDKVSQVVK 250

251 KGMECLQVEGTLKKS LDFKNDINAEAH SWGMKIYEDWAKNLTASQREALD 300
          ||:||||:||||| ||||| ||||| ||||| |||||:|.|.|||||
251 KGVECLQIEGTLKKS LDFKNDINAEAH SWGMKNYEEWAKDLTDSQREALD 300

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301 GYARQDYKEINNYLRNQGGSGNEKLDAQLKNISDALGKKPIPENITVYRW 350
      |||
301 GYARQDYKEINNYLRNQGGSGNEKLDAQIKNISDALGKKPIPENITVYRW 350
      |||

351 CGMPEFGYQISDPLPSLKD FEEQFLNTIKEDKGYMSTSLSSERLAAFGSR 400
      |||
351 CGMPEFGYQISDPLPSLKD FEEQFLNTIKEDKGYMSTSLSSERLAAFGSR 400
      |||

401 KIILRLQVPKGSTGAYLSAIGGFASEKEILLDKDSKYHIDKATEVIKGV 450
      |||
401 KIILRLQVPKGSTGAYLSAIGGFASEKEILLDKDSKYHIDKVTEVIKGV 450
      |||

451 KRYVVDATLLTN 462
      |||
451 KRYVVDATLLTN 462

```

TABLE 21

Alignment of VIP1 Amino Acid Sequences from *Bacillus thuringiensis* var.
tenebrionis (VIP1A(b)) vs. AB78 (VIP1A(a))

```

Btt      1 MKNMKKKLASVVTQMLLAPMFLNGNVNAV NADSKINQISTTQENQQKEMD 50 SEQ ID NO:21
      |||
Ab78     1 MKNMKKKLASVVTCTLLAPMFLNGNVNAV YADSKTNQISTTQKNQQKEMD 50 SEQ ID NO:5

51 RKGLLGYFFKGKDFNNLTMFAPTRDNTLMYDQQTANALLDKKQQEYQSIR 100
      |||
51 RKGLLGYFFKGKDFSNLTMFAPTRDSTLIYDQQTANKLLDKKQQEYQSIR 100

101 WIGLIQRKETGDFTFNLSKDEQAIIEIDGKIISNKGKEQVVHLEKEKLV 150
      |||
101 WIGLIQSKETGDFTFNLSEDEQAIIEINGKIISNKGKEQVVHLEKGLV 150

151 PIKIEYQSDTKFNIDSKTFKELKLFKIDSQNQSQQVQ...LRNPEFNKKE 197
      |||

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- 90 -

151 PIKIEYQSDTKFNIDSKTFKELKLFKIDSONQPQQVQQDELRNPEFNKKE 200

198 SQEFLAKASKTNLKFQKMKRDIDEDTDTGDSIPDLWEENGYTIQNKVAV 247
|||||:|.|||.||||:|||||:|||||:|

201 SQEFLAKPSKINLFTQKMKREIDEDTDTGDSIPDLWEENGYTIQNRIAV 250

248 KWDDSLASKGYTKFVSNPLDSHTVGDPTYDYEKAARDLDLSNAKETFNPL 297
|||||:|||||

251 KWDDSLASKGYTKFVSNPLESHTVGDPTYDYEKAARDLDLSNAKETFNPL 300

298 VAAFPSVNVSMKVLSPNENLSNSVESHSSTNWSYTNTEGASIEAGGGP 347
|||||:|||||

301 VAAFPSVNVSMKVLSPNENLSNSVESHSSTNWSYTNTEGASVEAGIGP 350

348 LGLSFGVSVTYQHSETVAQEWGTSTGNTSQFNTASAGYLNANVRYNNVGT 397
|:|||||.|||||

351 KGISFGVSVNYQHSETVAQEWGTSTGNTSQFNTASAGYLNANVRYNNVGT 400

398 GAIYDVKPTTSFVLNNTLIATITAKSNSTALRISPGDSYPEIGENAIAT 447
|||||:|||||.||||:|. |:|:|

401 GAIYDVKPTTSFVLNNDTLIATITAKSNSTALNISPGESYPKKGQNGIAIT 450

448 SMDDFNHPITLNKQOVNQLINNKPIMLETDQTDGVYKIRDTHGNIVTGG 497
|||||.|||.||:||||:||||:|||||

451 SMDDFNHPITLNKKQVDNLLNNKPMLETNQTDGVYKIKDTHGNIVTGG 500

498 EWNGVTQQIKAKTASIIVDDGKQVAEKRVAAKDYGHPEDKTPPLTLKDTL 547
|||||.|||||.|||||.||||:|||||.||||.

501 EWNGVIQQIKAKTASIIVDDGERVAEKRVAAKDYENPEDKTPSLTLKDAL 550

548 KLSYPDEIKETNGLLYYDDKPIYESSVMTYLDENTAKEVKKQINDTTGKF 597
|||||.|||.||:|||||.|||||.||:|||||

551 KLSYPDEIKEIEGLLYYKKNKPIYESSVMTYLDENTAKEVTKQINDTTGKF 600

VIP proteins may occur in nature as single polypeptides, or as two or more interacting polypeptides. When an active VIP is comprised of two or more interacting protein chains, these protein chains can be produced as a single polypeptide chain from a gene resulting from the fusion of the two (or more) VIP coding regions. The genes encoding the two chains are fused by merging the coding regions of the genes to produce a single open reading frame encoding both VIP polypeptides. The composite polypeptides can be fused to produce the smaller polypeptide as the NH₂ terminus of the fusion protein, or they can be fused to produce the larger of the

polypeptides as the NH₂ terminus of the fusion protein. A linker region can optionally be used between the two polypeptide domains. Such linkers are known in the art. This linker can optionally be designed to contain protease cleavage sites such that once the single fused polypeptide is ingested by the target insect it is cleaved in the linker region to liberate the two polypeptide components of the active VIP molecule.

VIP1A(a) and VIP2A(a) from *B. cereus* strain AB78 are fused to make a single polypeptide by fusing their coding regions. The resulting DNA comprises a sequence given in SEQ ID NO:22 with the encoded protein given in SEQ ID NO:23. In like manner, other fusion proteins may be produced.

The fusion of the genes encoding VIP1A(a) and VIP2A(a) is accomplished using standard techniques of molecular biology. The nucleotides deleted between the VIP1A(a) and VIP2A(a) coding regions are deleted using known mutagenesis techniques or, alternatively, the coding regions are fused using PCR techniques.

The fused VIP polypeptides can be expressed in other organisms using a synthetic gene, or partially synthetic gene, optimized for expression in the alternative host. For instance, to express the fused VIP polypeptide from above in maize, one makes a synthetic gene using the maize preferred codons for each amino acid, see for example EP-A 0618976, herein incorporated by reference. Synthetic DNA sequences created according to these methods are disclosed in SEQ ID NO:17 (maize optimized version of the 100 kDa VIP1A(a) coding sequence), SEQ ID NO:18 (maize optimized version of the 80 kDa VIP1A(a) coding sequence) and SEQ ID NO:24 (maize optimized version of the VIP2A(a) coding sequence).

Synthetic VIP1 and VIP2 genes optimized for expression in maize can be fused using PCR techniques, or the synthetic genes can be designed to be fused at a common restriction site. Alternatively, the synthetic fusion gene can be designed to encode a single polypeptide comprised of both VIP1 and VIP2 domains.

Addition of a peptide linker between the VIP1 and VIP2 domains of the fusion protein can be accomplished by PCR mutagenesis, use of a synthetic DNA linker encoding the linker peptide, or other methods known in the art.

The fused VIP polypeptides can be comprised of one or more binding domains. If more than one binding domain is used in the fusion, multiple target pests are controlled using such a fusion. The other binding domains can be obtained by using all or part of other VIPs; *Bacillus thuringiensis* endotoxins, or parts thereof; or other

proteins capable of binding to the target pest or appropriate binding domains derived from such binding proteins.

One example of a fusion construction comprising a maize optimized DNA sequence encoding a single polypeptide chain fusion having VIP2A(a) at the N-terminal end and VIP1A(a) at the C-terminal end is provided by pCIB5531. A DNA sequence encoding a linker with the peptide sequence PSTPPTPSPSTPPTPS (SEQ ID NO:47) has been inserted between the two coding regions. The sequence encoding this linker and relevant cloning sites is 5'- CCC GGG CCT TCT ACT CCC CCA ACT CCC TCT CCT AGC ACG CCT CCG ACA CCT AGC GAT ATC GGA TC C -3' (SEQ ID NO:48). Oligonucleotides were synthesized to represent both the upper and lower strands and cloned into a pUC vector following hybridization and phosphorylation using standard procedures. The stop codon in VIP2A(a) was removed using PCR and replaced by the BglII restriction site with a SmaI site. A translation fusion was made by ligating the Bam HI / PstI fragment of the VIP2A(a) gene from pCIB5522 (see Example 24), a PCR fragment containing the PstI-end fragment of the VIP2A(a) gene (identical to that used to construct pCIB5522), a synthetic linker having ends that would ligate with a blunt site at the 5' end and with BamHI at the 3' end and the modified synthetic VIP1A(a) gene from pCIB5526 described below (See SEQ ID NO:35). The fusion was obtained by a four way ligation that resulted in a plasmid containing the VIP2A(a) gene without a translation stop codon, with a linker and the VIP1A(a) coding region without the *Bacillus* secretion signal. The DNA sequence for this construction is disclosed in SEQ ID NO:49, which encodes the fusion protein disclosed in SEQ ID NO:50. A single polypeptide fusion where VIP1A(a) is at the N-terminal end and VIP2A(a) is at the C-terminal end can be made in a similar fashion. Furthermore, either one or both genes can be linked in a translation fusion with or without a linker at either the 5' or the 3' end to other molecules like toxin encoding genes or reporter genes.

EXAMPLE 23. TARGETING OF VIP2 TO PLANT ORGANELLES

Various mechanisms for targeting gene products are known to exist in plants and the sequences controlling the functioning of these mechanisms have been characterized in some detail. For example, the targeting of gene products to the

chloroplast is controlled by a signal sequence found at the amino-terminal end of various proteins. This signal is cleaved during chloroplast import, yielding the mature protein (*e.g.* Comai *et al.* J. Biol. Chem. 263: 15104-15109 (1988)). These signal sequences can be fused to heterologous gene products such as VIP2 to effect the import of those products into the chloroplast (van den Broeck *et al.* Nature 313: 358-363 (1985)). DNA encoding for appropriate signal sequences can be isolated from the 5' end of the cDNAs encoding the RUBISCO protein, the CAB protein, the EPSP synthase enzyme, the GS2 protein and many other proteins which are known to be chloroplast localized.

Other gene products are localized to other organelles such as the mitochondrion and the peroxisome (*e.g.* Unger *et al.* Plant Molec. Biol. 13: 411-418 (1989)). The cDNAs encoding these products can also be manipulated to effect the targeting of heterologous gene products such as VIP2 to these organelles. Examples of such sequences are the nuclear-encoded ATPases and specific aspartate amino transferase isoforms for mitochondria. Similarly, targeting to cellular protein bodies has been described by Rogers *et al.* (Proc. Natl. Acad. Sci. USA 82: 6512-6516 (1985)).

By the fusion of the appropriate targeting sequences described above to coding sequences of interest such as VIP2 it is possible to direct the transgene product to any organelle or cell compartment. For chloroplast targeting, for example, the chloroplast signal sequence from the RUBISCO gene, the CAB gene, the EPSP synthase gene, or the GS2 gene is fused in frame to the amino-terminal ATG of the transgene. The signal sequence selected should include the known cleavage site and the fusion constructed should take into account any amino acids after the cleavage site which are required for cleavage. In some cases this requirement may be fulfilled by the addition of a small number of amino acids between the cleavage site and the start codon ATG, or alternatively replacement of some amino acids within the coding sequence. Fusions constructed for chloroplast import can be tested for efficacy of chloroplast uptake by *in vitro* translation of *in vitro* transcribed constructions followed by *in vitro* chloroplast uptake using techniques described by (Bartlett *et al.* In: Edelman *et al.* (Eds.) Methods in Chloroplast Molecular Biology, Elsevier. pp 1081-1091 (1982); Wasmann *et al.* Mol. Gen. Genet. 205: 446-453 (1986)). These

construction techniques are well known in the art and are equally applicable to mitochondria and peroxisomes.

The above described mechanisms for cellular targeting can be utilized not only in conjunction with their cognate promoters, but also in conjunction with heterologous promoters so as to effect a specific cell targeting goal under the transcriptional regulation of a promoter which has an expression pattern different to that of the promoter from which the targeting signal derives.

A DNA sequence encoding a secretion signal is present in the native *Bacillus* VIP2 gene. This signal is not present in the mature protein which has the N-terminal sequence of LKITDKVEDF (amino acid residues 57 to 66 of SEQ ID NO:2). It is possible to engineer VIP2 to be secreted out of the plant cell or to be targeted to subcellular organelles such as the endoplasmic reticulum, vacuole, mitochondria or plastids including chloroplasts. Hybrid proteins made by fusion of a secretion signal peptide to a marker gene have been successfully targeted into the secretion pathway. (Itirriaga G. *et al.*, The Plant Cell, 1: 381-390 (1989) , Denecke *et al.*, The Plant Cell, 2:51-59 (1990). Amino-terminal sequences have been identified that are responsible for targeting to the ER, the apoplast, and extracellular secretion from aleurone cells (Koehler & Ho, Plant Cell 2: 769-783 (1990)).

The presence of additional signals are required for the protein to be retained in the endoplasmic reticulum or the vacuole. The peptide sequence KDEL/HDEL at the carboxy-terminal of a protein is required for its retention in the endoplasmic reticulum (reviewed by Pelham, Annual Review Cell Biol., 5:1-23 (1989). The signals for retention of proteins in the vacuole have also been characterized. Vacuolar targeting signals may be present either at the amino-terminal portion, (Holwerda *et al.*, The Plant Cell, 4:307-318 (1992), Nakamura *et al.*, Plant Physiol., 101:1-5 (1993)), carboxy- terminal portion, or in the internal sequence of the targeted protein. (Tague *et al.*, The Plant Cell, 4:307-318 (1992), Saalbach *et al.*, The Plant Cell, 3:695-708 (1991)). Additionally, amino-terminal sequences in conjunction with carboxy-terminal sequences are responsible for vacuolar targeting of gene products (Shinshi *et al.* Plant Molec. Biol. 14: 357-368 (1990)). Similarly, proteins may be targeted to the mitochondria or plastids using specific carboxy terminal signal peptide fusions (Heijne *et al.*, Eur. J. Biochem., 180:535-545 (1989), Archer and Keegstra, Plant Molecular Biology, 23:1105-1115 (1993)).

In order to target VIP2, either for secretion or to the various subcellular organelles, a maize optimized DNA sequence encoding a known signal peptide(s) may be designed to be at the 5' or the 3' end of the gene as required. To secrete VIP2 out of the cell, a DNA sequence encoding the eukaryotic secretion signal peptide MGWSWIFLFLLSGAAGVHCL (SEQ ID NO:25) from PCT application No. IB95/00497 or any other described in the literature (Itirriaga *et al.*, The Plant Cell, 1:381-390 (1989), Denecke, *et al.*, The Plant Cell, 2:51-59 (1990)) may be added to the 5' end of either the complete VIP2 gene sequence or to the sequence truncated to encode the mature protein or the gene truncated to nucleotide 286 or encoding a protein to start at amino acid residue 94 (methionine). To target VIP2 to be retained in the endoplasmic reticulum, a DNA sequence encoding the ER signal peptide KDEL/HDEL, in addition to the secretion signal, can be added to the 3' end of the gene. For vacuolar targeting a DNA sequence encoding the signal peptide SSSSFADSNPIRVTDRAAST (SEQ ID NO:3; Holwerda *et al.*, The Plant Cell, 4:307-318 (1992)) can be designed to be adjacent to the secretion signal or a sequence encoding a carboxyl signal peptide as described by Dombrowski *et al.*, The Plant Cell, 5:587-596 (1993) or a functional variation may be inserted at the 3' end of the gene. Similarly, VIP2 can be designed to be targeted to either the mitochondria or the plastids, including the chloroplasts, by inserting sequences in the VIP2 sequence described that would encode the required targeting signals. The bacterial secretion signal present in VIP2 may be retained or removed from the final construction.

One example of a construction which incorporates a eukaryotic secretion signal fused to a coding sequence for a VIP is provided by pCIB5528. Oligonucleotides corresponding to both the upper and lower strand of sequences encoding the secretion signal peptide of SEQ ID NO:25 was synthesized and has the sequence 5'-GGATCCACC ATG GGC TGG AGC TGG ATC TTC CTG TTC CTG CTG AGC GGC GCC GCG GGC GTG CAC TGC CTGCAG-3' (SEQ ID NO:41). When hybridized, the 5' end of the secretion signal resembled "sticky-ends" corresponding to restriction sites BamHI and PstI. The oligonucleotide was hybridized and phosphorylated and ligated into pCIB5527 (construction described in Example 23A) which had been digested with BamHI/ PstI using standard procedures. The resulting maize optimized coding sequence is disclosed in SEQ ID NO:42 which encodes the protein disclosed

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in SEQ ID NO:43. This encoded protein comprises the eukaryotic secretion signal in place of the *Bacillus* secretion signal.

One example of a construction which incorporates a vacuolar targetting signal fused to a coding sequence for a VIP is provided by pCIB5533. Oligonucleotides corresponding to both the upper and lower strand of sequences encoding the vacuolar targetting peptide of SEQ ID NO:3 was synthesized and has the sequence 5'-CCG CCG GCG TGC ACT GCC TCA GCA GCA GCA GCT TCG CCG ACA GCA ACC CCA TCC GCG TGA CCG ACC GCG CCG CCA GCA CCC TGC AG-3' (SEQ ID NO:44). When hybridized, the 5' end of the vacuolar targetting signal resembled "sticky-ends" corresponding to restriction sites SacII and PstI. The oligonucleotide was hybridized and phosphorylated and ligated into pCIB5528 (construction described above) which had been digested with SacII / PstI using standard procedures. The resulting maize optimized coding sequence is disclosed in SEQ ID NO:45 which encodes the protein disclosed in SEQ ID NO:46. This encoded protein comprises the vacuolar targetting peptide in addition to the eukaryotic secretion signal.

The VIP1 gene can also be designed to be secreted or targeted to subcellular organelles by similar procedures.

EXAMPLE 23A. REMOVAL OF *BACILLUS* SECRETION SIGNAL FROM VIP1A(a) AND VIP2A(a)

VIP1A(a) and VIP2A(a) are secreted during the growth of strain AB78. The nature of peptide sequences that act as secretion signals has been described in the literature (Simonen and Palva, Microbiological reviews, pg. 109-137 (1993)). Following the information in the above publication, the putative secretion signal was identified in both genes. In VIP1A(a) this signal is composed of amino acids 1-33 (See SEQ ID NO:5). Processing of the secretion signal probably occurs after the serine at amino acid 33. The secretion signal in VIP2A(a) was identified as amino acids 1-49 (See SEQ ID NO:2). N-terminal peptide analysis of the secreted mature VIP2A(a) protein revealed the N-terminal sequence LKITDKVEDFKEDK. This sequence is found beginning at amino acid 57 in SEQ ID NO:2. The genes encoding these proteins have been modified by removal of the *Bacillus* secretion signals.

A maize optimized VIP1A(a) coding region was constructed which had the sequences encoding the first 33 amino acids, i.e., the secretion signal, removed from its 5' end. This modification was obtained by PCR using an forward primer that

contained the sequence 5'-GGA TCC ACC ATG AAG ACC AAC CAG ATC AGC-3' (SEQ ID NO:33), which hybridizes with the maize optimized gene (SEQ ID NO:26) at nucleotide position 100, and added a BamHI restriction site and a eukaryotic translation start site consensus including a start codon. The reverse primer that contained the sequence 5'-AAG CTT CAG CTC CTT G-3' (SEQ ID NO:34) hybridizes on the complementary strand at nucleotide position 507. A 527 bp amplification product was obtained containing the restriction sites BamHI at the 5' end and HindIII site at the 3' end. The amplification product was cloned into a T- vector (described in Example 24, below) and sequenced to ensure the correct DNA sequence. The BamHI / HindIII fragment was then obtained by restriction digest and used to replace the BamHI/HindIII fragment of the maize optimized VIP1A(a) gene cloned in the root-preferred promoter cassette. The construct obtained was designated pCIB5526. The maize optimized coding region for VIP1A(a) with the *Bacillus* secretion signal removed is disclosed as SEQ ID NO:35 and the encoded protein is disclosed as SEQ ID NO:36.

The gene encoding the processed form of VIP2A(a), i.e., a coding region with the secretion signal removed, was constructed by a procedure similar to that described for that used to construct the processed form of VIP1A(a), above. The modification was obtained by PCR using the forward primer 5'-GGA TCC ACC ATG CTG CAG AAC CTG AAG ATC AC -3' (SEQ ID NO:37). This primer hybridizes at nucleotide position 150 of the maize optimized VIP2A(a) gene (SEQ ID NO:27). A silent mutation has been inserted at nucleotide position 15 of this primer to obtain a PstI restriction site. The reverse primer has the sequence 5'-AAG CTT CCA CTC CTT CTC-3' (SEQ ID NO:38). A 259 bp product was obtained with HindIII restriction site at the 3' end. The amplification product was cloned into a T- vector, sequenced and ligated to a BamHI /HindIII digested root-preferred promoter cassette containing the maize optimized VIP2A(a). The construct obtained was designated pCIB5527. The maize optimized coding region for VIP2A(a) with the *Bacillus* secretion signal removed is disclosed as SEQ ID NO:39 and the encoded protein is disclosed as SEQ ID NO:40.

EXAMPLE 24. CONSTRUCTION AND CLONING OF THE VIP1A(a) AND VIP2A(a) MAIZE OPTIMIZED GENES

Design: The maize optimized genes were designed by reverse translation of the native VIP1A(a) and VIP2A(a) protein sequences using codons that are used most often in maize (Murray *et al.*, Nucleic Acid Research, 17:477-498 (1989)). To facilitate cloning, the DNA sequence was further modified to incorporate unique restriction sites at intervals of every 200-360 nucleotides. VIP1A(a) was designed to be cloned in 11 such fragments and VIP2A(a) was cloned in 5 fragments. Following cloning of the individual fragments, adjacent fragments were joined using the restriction sites common to both fragments, to obtain the complete gene. To clone each fragment, oligonucleotides (50-85 nucleotides) were designed to represent both the upper and the lower strand of the DNA. The upper oligo of the first oligo pair was designed to have a 15 bp single stranded region at the 3' end which was homologous to a similar single stranded region of the lower strand of the next oligo pair to direct the orientation and sequence of the various oligo pairs within a given fragment. The oligos are also designed such that when all the oligos representing a fragment are hybridized, the ends have single stranded regions corresponding to the particular restriction site to be formed. The structure of each oligomer was examined for stable secondary structures such as hairpin loops using the OLIGO program from NBI Inc. Whenever necessary, nucleotides were changed to decrease the stability of the secondary structure without changing the amino acid sequence of the protein. A plant ribosomal binding site consensus sequence, TAAACAATG (Joshi *et al.*, Nucleic Acid Res., 15:6643-6653 (1987)) or eukaryotic ribosomal binding site consensus sequence CCACCATG (Kozak, Nucleic Acid Research, 12:857-872 (1984)) was inserted at the translational start codon of the gene.

Cloning: Oligos were synthesized by IDT Inc., and were supplied as lyophilized powders. They were resuspended at a concentration of 200 µM. To 30 µl of each oligo formamide was added a final concentration of 25-50% and the sample was boiled for two minutes before separation on a premade 10% polyacrylamide / urea gel obtained from Novex. After electrophoresis, the oligo was detected by UV shadowing by placing the gel on a TLC plate containing a fluorescent indicator and exposing it to UV light. The region containing DNA of the correct size was excised and extracted

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from the polyacryamide by an overnight incubation of the minced gel fragment in a buffer containing 0.4 M LiCl, 0.1 mM EDTA. The DNA was separated from the gel residue by centrifugation through a Millipore UPMC filter. The extracted DNA was ethanol precipitated by the addition of 2 volumes of absolute alcohol. After centrifugation, the precipitate was resuspended in dH₂O at a concentration of 2.5 µM. Fragments were cloned either by hybridization of the oligos and ligation with the appropriate vector or by amplification of the hybridized fragment using a equimolar mixture of all the oligos for a particular fragment as a template and end-specific PCR primers.

Cloning by hybridization and ligation: Homologous double stranded oligo pairs were obtained by mixing 5 µl of the upper and of the lower oligo for each oligo pair with buffer containing 1X polynucleotide kinase (PNK) buffer (70 mM Tris-HCl (pH 7.6), 10 mM MgCl₂, 5 mM dithiothreitol (DTT)), 50 mM KCl, and 5 % formamide in a final volume of 50 µl. The oligos were boiled for 10 minutes and slow cooled to 37° C or room temperature. 10 µl was removed for analysis on a 4% agarose in a TAE buffer system (Metaphore®; FMC). Each hybridized oligo pair was kinased by the addition of ATP at a final concentration of 1 mM, BSA at a final concentration of 100 µg per ml and 200 units of polynucleotide kinase and 1 µl of 10X PNK buffer in a volume of 10 µl. Following hybridization and phosphorylation, the reaction was incubated at 37° C for 2 hours to overnight. 10 µl of each of the oligo pairs for a particular fragment, were mixed in a final volume of 50 µl. The oligo pairs were hybridized by heating at 80° C for 10 minutes and slow cooling to 37° C. 2 µl of oligos was mixed with about 100 ng of an appropriate vector and ligated using a buffer containing 50 mM Tris-HCl (pH 7.8), 10 mM MgCl₂, 10 mM DTT, 1 mM ATP. The reaction was incubated at room temp. for 2 hours to overnight and transformed into DH5α strain of *E.coli*, plated on L- plates containing ampicillin at a concentration of 100 µg/ml using standard procedures. Positive clones were further characterized and confirmed by PCR miniscreen described in detail in EP-A 0618976 using the universal primers "Reverse" and M13 "-20 " as primers. Positive clones were identified by digestion of DNA with appropriate enzymes followed by sequencing. Recombinants that had the expected DNA sequence were then selected for further work.

PCR Amplification and cloning into T- vector:

PCR amplification was carried out by using a mixture of all the oligomers that represented the upper and the lower strand of a particular fragment (final concentration 5 mM each) as template, specific end primers for the particular fragment (final concentration 2 μ M) 200 μ M of each dATP, dTTP, dCTP and dGTP, 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1.5 mM MgCl₂, 0.01% gelatin and 5 units of Taq polymerase in a final reaction volume of 50 μ l. The amplification reaction was carried out in a Perkin Elmer thermocycler 9600 by incubation at 95° C for 1 min (1 cycle), followed by 20 cycles of 95 °C for 45 sec., 50 °C for 45 sec., 72 °C for 30 sec. Finally the reaction was incubated for 5 min at 72°C before analyzing the product. 10 μ l of the reaction was analyzed on a 2.5% Nusieve (FMC) agarose gel in a TAE buffer system. The correct size fragment was gel purified and used for cloning into a PCR cloning vector or T-vector. T-vector construction was as described by Marchuk *et al.*, Nucleic Acid Research, 19:1154 (1991). pBluescriptsk+ (Stratagene®, Ca.) was used as the parent vector. Transformation and identification of the correct clone was carried out as described above.

Fragments 1, 3, 4, 5, 6, 8, and 9 of VIP1A(a) and fragments 2 and 4 of VIP2A(a) were obtained by cloning of PCR amplification products; whereas, fragments 2, 7, 10 and 11 of VIP1A(a) and fragments 1, 3, and 5 of VIP2A(a) were obtained by hybridization/ ligation.

Once fragments with the desired sequence were obtained, the complete gene was assembled by cloning together adjacent fragments. The complete gene was resequenced and tested for activity against WCRW before moving it into plant expression vectors containing the root preferred promoter (disclosed in U.S. patent application serial no. 08/017,209, herein incorporated by reference) and the rice actin promoter.

One such plant expression vector is pCIB5521. The maize optimized VIP1A(a) coding region (SEQ ID NO:26) was cloned in a plant expression vector containing the root preferred promoter at the 5' of the gene with the PEP Carboxylase intron #9 followed by the 35S terminator at the 3' end. The plasmid also contains sequences for ampicillin resistance from the plasmid pUC19. Another plant expression vector is pCIB5522, which contains the maize optimized VIP2A(a) coding region (SEQ ID

NO:27) fused to the root preferred promoter at the 5' of the gene with the PEP Carboxylase intron #9 followed by the 35S terminator at the 3' end.

EXAMPLE 25. NAD AFFINITY CHROMATOGRAPHY

A purification strategy was used based on the affinity of VIP2 for the substrate NAD. The supernatant from the pH 3.5 sodium citrate buffer treatment described in Example 4 was dialyzed in 20 mM TRIS pH 7.5 overnight. The neutralized supernatant was added to an equal volume of washed NAD agarose and incubated with gentle rocking at 4° C overnight. The resin and protein solution were added to a 10 ml disposable polypropylene column and the protein solution allowed to flow out. The column was washed with 5 column volumes of 20 mM TRIS pH 7.5 then washed with 2-5 column volumes of 20 mM TRIS pH 7.5, 100 mM NaCl, followed by 2-5 column volumes of 20 mM TRIS 7.5. The VIP proteins were eluted in 20 mM TRIS pH 7.5 supplemented with 5 mM NAD. Approximately 3 column volumes of the effluent were collected and concentrated in a Centricon -10. Yield is typically about 7-15 µg of protein per ml of resin.

When the purified proteins were analyzed by SDS-PAGE followed by silver staining, two polypeptides were visible, one with Mr of approximately 80,000 and one with Mr of approximately 45,000. N-terminal sequencing revealed that the Mr 80,000 protein corresponded to a proteolytically processed form of VIP1A(A) and the Mr 45,000 form corresponded to a proteolytically processed form of VIP2A(a). The co-purification of VIP1A(a) with VIP2A(a) indicates that the two proteins probably form a complex and have protein-protein interacting regions. VIP1A(a) and VIP2A(a) proteins purified in this manner were biologically active against western corn rootworm.

EXAMPLE 26. EXPRESSION OF MAIZE OPTIMIZED VIP1A(a) AND VIP2A(a)

E. coli strains containing different plasmids comprising VIP genes were assayed for expression of VIPs. *E. coli* strains harboring the individual plasmids were grown overnight in L-broth and expressed protein was extracted from the culture as described in Example 3, above. Protein expression was assayed by Western Blot analysis using antibodies developed using standard methods known in the art, similar

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to those described in Example 12, above. Also, insecticidal activity of the expressed proteins were tested against Western corn rootworm according to the method in Example 3, above. The results of the *E. coli* expression assays are described below.

Expression of VIPs in *E. coli*

Extract of <i>E. coli</i> Strain Harboring Indicated Plasmid	Assay No. 1	Assay No. 2	Protein Detected
	% Mortality		
Control	0	0	no
pCIB5521 (maize optimized VIP1A(a))	47	27	yes
pCIB5522 (maize optimized VIP2A(a))	7	7	yes
pCIB6024 (native VIP2A(a))	13	13	yes
pCIB6206 (native VIP1A(a))	27	40	yes
Extracts pCIB5521 + pCIB5522 combined	87	47	
Extracts pCIB5521 + pCIB6024 combined	93	100	
Extracts pCIB5522 + pCIB6206 combined	100	100	
Extracts pCIB6024 + pCIB6206 combined	100	100	

The DNA from these plasmids was used to transiently express the VIPs in a maize protoplast expression system. Protoplasts were isolated from maize 2717 Line 6 suspension cultures by digestion of the cell walls using Cellulase RS and Macerase R10 in appropriate buffer. Protoplasts were recovered by sieving and centrifugation. Protoplasts were transformed by a standard direct gene transfer method using approximately 75 µg plasmid DNA and PEG-40. Treated protoplasts were incubated overnight in the dark at room temperature. Analysis of VIP expression was

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accomplished on protoplast explants by Western blot analysis and insecticidal activity against Western corn rootworm as described above for the expression in *E. coli*. The results of the maize protoplast expression assays are described below.

Expression of VIPs in Plant Protoplasts

<i>Extract Tested</i>	<i>Assay No. 1</i>	<i>Assay No. 2</i>	<i>Protein Detected</i>
	% Mortality		
No DNA control	27	10	no
pCIB5521 (p) (maize optimized VIP1A(a))	20 (0)	30	yes
pCIB5522 (p) (maize optimized VIP2A(a))	20 (0)	20	yes
Extracts pCIB5521 (p) + pCIB5522 (p) combined	87 (82)	90	
Extracts pCIB5521 (p) + pCIB5522 (e) combined	100	-	
Extracts pCIB5522 (p) + pCIB5521 (e) combined	53 (36)	-	
Extracts pCIB5521 (p) + pCIB6024 (e) combined	100	-	
Extracts pCIB5522 (p) + pCIB6206 (e) combined	100	-	
pCIB6024(e) (native VIP2A(a))	0	-	yes
pCIB6206(e) (native VIP1A(a))	20	-	yes
pCIB5521 + pCIB 5522 (plasmids delivered by cotransformation)	100	100	yes

(p) = extract of protoplast culture transformed with indicated plasmid

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(e) = extract of *E. coli* strain harboring indicated plasmid

The expression data obtained with both *E. coli* and maize protoplasts show that the maize optimized VIP1A(a) and VIP2A(a) genes make the same protein as the native VIP1A(a) and VIP2A(a) genes, respectively, and that the proteins encoded by the maize optimized genes are functionally equivalent to the proteins encoded by the native genes.

All publications and patent applications mentioned in this specification are indicative of the level of skill of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

The following deposits have been made at Agricultural Research Service, Patent Culture Collection (NRRL), Northern Regional Research Center, 1815 North University Street, Peoria, Illinois 61604, USA:

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Strain designation		Deposition Number	Deposition Date
1.	<i>E. coli</i> PL2	NRRL B-21221	March 09, 1994
2.	<i>E. coli</i> PL2	NRRL B-21221N	September 02, 1994
3.	<i>E. coli</i> pCIB6022	NRRL B-21222	March 09, 1994
4.	<i>E. coli</i> pCIB6023	NRRL B-21223	March 09, 1994
5.	<i>E. coli</i> pCIB6023	NRRL B-21223N	September 02, 1994
6.	<i>Bacillus thuringiensis</i> HD73-78VIP	NRRL B-21224	March 09, 1994
7.	<i>Bacillus thuringiensis</i> AB88	NRRL B-21225	March 09, 1994
8.	<i>Bacillus thuringiensis</i> AB359	NRRL B-21226	March 09, 1994
9.	<i>Bacillus thuringiensis</i> AB289	NRRL B-21227	March 09, 1994
10.	<i>Bacillus</i> sp. AB59	NRRL B-21228	March 09, 1994
11.	<i>Bacillus</i> sp. AB294	NRRL B-21229	March 09, 1994
12.	<i>Bacillus</i> sp. AB256	NRRL B-21230	March 09, 1994
13.	<i>E. coli</i> P5-4	NRRL B-21059	March 18, 1993
14.	<i>E. coli</i> P3-12	NRRL B-21061	March 18, 1993
15.	<i>Bacillus cereus</i> AB78	NRRL B-21058	March 18, 1993
16.	<i>Bacillus thuringiensis</i> AB6	NRRL B-21060	March 18, 1993
17.	<i>E. coli</i> pCIB6202	NRRL B-21321	September 02, 1994
18.	<i>E. coli</i> pCIB7100	NRRL B-21322	September 02, 1994
19.	<i>E. coli</i> pCIB7101	NRRL B-21323	September 02, 1994
20.	<i>E. coli</i> pCIB7102	NRRL B-21324	September 02, 1994
21.	<i>E. coli</i> pCIB7103	NRRL B-21325	September 02, 1994
22.	<i>E. coli</i> pCIB7104	NRRL B-21422	March 24, 1995
23.	<i>E. coli</i> pCIB7107	NRRL B-21423	March 24, 1995
24.	<i>E. coli</i> pCIB7108	NRRL B-21438	May 05, 1995
25.	<i>Bacillus thuringiensis</i> AB424	NRRL B-21439	May 05, 1995

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (A) NAME: CIBA-GEIGY AG
- (B) STREET: Klybeckstr. 141
- (C) CITY: Basel
- (E) COUNTRY: Switzerland
- (F) POSTAL CODE (ZIP): 4002
- (G) TELEPHONE: +41 61 69 11 11
- (H) TELEFAX: + 41 61 696 79 76
- (I) TELEX: 962 991

(ii) TITLE OF INVENTION: Novel Pesticidal Proteins and Strains

(iii) NUMBER OF SEQUENCES: 52

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30B

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Bacillus cereus
- (B) STRAIN: AB78
- (C) INDIVIDUAL ISOLATE: NRRL B-21058

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1082..2467
- (D) OTHER INFORMATION: /product= "VIP2A(a)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 2475..5126
- (D) OTHER INFORMATION: /note= "Coding sequence for the 100 kd VIP1A(a) protein. This coding sequence is repeated in SEQ ID NO:4 and translated separately."

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATCGATACAA TGTGTTTTTA CTTAGACCGG TAGTCTCTGT AATTTGTTTA ATGCTATATT	60
CTTTACTTTG ATACATTTTA ATAGCCATTT CAACCTTATC AGTATGTTTT TGTGGTCTTC	120
CTCCTTTTTT TCCACGAGCT CTAGCTGCGT TTAATCCTGT TTTGGTACGT TCGCTAATAA	180
TATCTCTTTC TAATTCTGCA ATACTTGCCA TCATTGCGAA GAAGAATTTT CCCATAGCAT	240
TAGAGGTATC AATGTTGTCA TGAATAGAAA TAAATCTAC ACCTAGCTCT TTGAATTTTT	300
CACTTAACTC AATTAGGTGT TTTGTAGAGC GAGAAATTCG ATCAAGTTTG TAAACAATA	360
TCTTATCGCC TTTACGTAAT ACTTTTAGCA ACTCTTCGAG TTGAGGGCGC TCTTTTTTTA	420
TTCTGTATAT TTTCTCCTGA TATAGCCTTT CTACACCATA TTGTTGCAA GCATCTATTT	480
GCATATCGAG ATTTTGTTC TCTGTGCTGA CACGAGCATA ACCAAAAATC AAATTGGTTT	540
CACTTCCTAT CTAAATATAT CTATTAAAAT AGCACCAAAA ACCTTATTAA ATTAAAAATA	600
GGAACCTTGT TTTTGGATAT GGATTTTGGT ACTCAATATG GATGAGTTTT TAACGCTTTT	660
GTAAAAAAC AAACAAGTGC CATAAACGGT CGTTTTTGGG ATGACATAAT AAATAATCTG	720
TTTGATTAAC CTAACCTTGT ATCCTTACAG CCCAGTTTTA TTTGTACTTC AACTGACTGA	780
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CTTTAGGTTA TAGTTAAATT ATAAGAAAAA AACAAACGGA GGGAGTGAAA AAAAGCATCT	900
TCTCTATAAT TTTACAGGCT CTTTAATAAG AAGGGGGGAG ATTAGATAAT AAATATGAAT	960
ATCTATCTAT AATTGTTTGC TTCTACAATA ACTTATCTAA CTTTCATATA CAACAACAAA	1020
ACAGACTAAA TCCAGATTGT ATATTCATTT TCAGTTGTTT CTTTATAAAA TAATTTTATA	1080
A ATG AAA AGA ATG GAG GGA AAG TTG TTT ATG GTG TCA AAA AAA TTA	1126
Met Lys Arg Met Glu Gly Lys Leu Phe Met Val Ser Lys Lys Leu	
1 5 10 15	
CAA GTA GTT ACT AAA ACT GTA TTG CTT AGT ACA GTT TTC TCT ATA TCT	1174
Gln Val Val Thr Lys Thr Val Leu Leu Ser Thr Val Phe Ser Ile Ser	
20 25 30	
TTA TTA AAT AAT GAA GTG ATA AAA GCT GAA CAA TTA AAT ATA AAT TCT	1222
Leu Leu Asn Asn Glu Val Ile Lys Ala Glu Gln Leu Asn Ile Asn Ser	
35 40 45	
CAA AGT AAA TAT ACT AAC TTG CAA AAT CTA AAA ATC ACT GAC AAG GTA	1270
Gln Ser Lys Tyr Thr Asn Leu Gln Asn Leu Lys Ile Thr Asp Lys Val	
50 55 60	
GAG GAT TTT AAA GAA GAT AAG GAA AAA GCG AAA GAA TGG GGG AAA GAA	1318

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Glu Asp Phe Lys Glu Asp Lys Glu Lys Ala Lys Glu Trp Gly Lys Glu	
65 70 75	
AAA GAA AAA GAG TGG AAA CTA ACT GCT ACT GAA AAA GGA AAA ATG AAT	1366
Lys Glu Lys Glu Trp Lys Leu Thr Ala Thr Glu Lys Gly Lys Met Asn	
80 85 90 95	
AAT TTT TTA GAT AAT AAA AAT GAT ATA AAG ACA AAT TAT AAA GAA ATT	1414
Asn Phe Leu Asp Asn Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile	
100 105 110	
ACT TTT TCT ATG GCA GGC TCA TTT GAA GAT GAA ATA AAA GAT TTA AAA	1462
Thr Phe Ser Met Ala Gly Ser Phe Glu Asp Glu Ile Lys Asp Leu Lys	
115 120 125	
GAA ATT GAT AAG ATG TTT GAT AAA ACC AAT CTA TCA AAT TCT ATT ATC	1510
Glu Ile Asp Lys Met Phe Asp Lys Thr Asn Leu Ser Asn Ser Ile Ile	
130 135 140	
ACC TAT AAA AAT GTG GAA CCG ACA ACA ATT GGA TTT AAT AAA TCT TTA	1558
Thr Tyr Lys Asn Val Glu Pro Thr Thr Ile Gly Phe Asn Lys Ser Leu	
145 150 155	
ACA GAA GGT AAT ACG ATT AAT TCT GAT GCA ATG GCA CAG TTT AAA GAA	1606
Thr Glu Gly Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu	
160 165 170 175	
CAA TTT TTA GAT AGG GAT ATT AAG TTT GAT AGT TAT CTA GAT ACG CAT	1654
Gln Phe Leu Asp Arg Asp Ile Lys Phe Asp Ser Tyr Leu Asp Thr His	
180 185 190	
TTA ACT GCT CAA CAA GTT TCC AGT AAA GAA AGA GTT ATT TTG AAG GTT	1702
Leu Thr Ala Gln Gln Val Ser Ser Lys Glu Arg Val Ile Leu Lys Val	
195 200 205	
ACG GTT CCG AGT GGG AAA GGT TCT ACT ACT CCA ACA AAA GCA GGT GTC	1750
Thr Val Pro Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val	
210 215 220	
ATT TTA AAT AAT AGT GAA TAC AAA ATG CTC ATT GAT AAT GGG TAT ATG	1798
Ile Leu Asn Asn Ser Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Met	
225 230 235	
GTC CAT GTA GAT AAG GTA TCA AAA GTG GTG AAA AAA GGG GTG GAG TGC	1846
Val His Val Asp Lys Val Ser Lys Val Val Lys Lys Gly Val Glu Cys	
240 245 250 255	
TTA CAA ATT GAA GGG ACT TTA AAA AAG AGT CTT GAC TTT AAA AAT GAT	1894
Leu Gln Ile Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp	
260 265 270	
ATA AAT GCT GAA GCG CAT AGC TGG GGT ATG AAG AAT TAT GAA GAG TGG	1942
Ile Asn Ala Glu Ala His Ser Trp Gly Met Lys Asn Tyr Glu Glu Trp	
275 280 285	

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GCT AAA GAT TTA ACC GAT TCG CAA AGG GAA GCT TTA GAT GGG TAT GCT Ala Lys Asp Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala 290 295 300	1990
AGG CAA GAT TAT AAA GAA ATC AAT AAT TAT TTA AGA AAT CAA GGC GGA Arg Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly 305 310 315	2038
AGT GGA AAT GAA AAA CTA GAT GCT CAA ATA AAA AAT ATT TCT GAT GCT Ser Gly Asn Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala 320 325 330 335	2086
TTA GGG AAG AAA CCA ATA CCG GAA AAT ATT ACT GTG TAT AGA TGG TGT Leu Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys 340 345 350	2134
GGC ATG CCG GAA TTT GGT TAT CAA ATT AGT GAT CCG TTA CCT TCT TTA Gly Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu 355 360 365	2182
AAA GAT TTT GAA GAA CAA TTT TTA AAT ACA ATC AAA GAA GAC AAA GGA Lys Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly 370 375 380	2230
TAT ATG AGT ACA AGC TTA TCG AGT GAA CGT CTT GCA GCT TTT GGA TCT Tyr Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser 385 390 395	2278
AGA AAA ATT ATA TTA CGA TTA CAA GTT CCG AAA GGA AGT ACG GGT GCG Arg Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala 400 405 410 415	2326
TAT TTA AGT GCC ATT GGT GGA TTT GCA AGT GAA AAA GAG ATC CTA CTT Tyr Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu 420 425 430	2374
GAT AAA GAT AGT AAA TAT CAT ATT GAT AAA GTA ACA GAG GTA ATT ATT Asp Lys Asp Ser Lys Tyr His Ile Asp Lys Val Thr Glu Val Ile Ile 435 440 445	2422
AAA GGT GTT AAG CGA TAT GTA GTG GAT GCA ACA TTA TTA ACA AAT Lys Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn 450 455 460	2467
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TCCTATGTTT TTGAATGGAA ATGTGAATGC TGTTTACGCA GACAGCAAAA CAAATCAAAT	2587
TTCTACAACA CAGAAAAATC AACAGAAAGA GATGGACCGA AAAGGATTAC TTGGGTATTA	2647
TTTCAAAGGA AAAGATTTTA GTAATCTTAC TATGTTTGCA CCGACACGTG ATAGTACTCT	2707
TATTTATGAT CAACAAACAG CAAATAAACT ATTAGATAAA AAACAACAAG AATATCAGTC	2767
TATTCGTTGG ATTGGTTTGA TTCAGAGTAA AGAAACGGGA GATTTCACAT TTAACCTTATC	2827

TGAGGATGAA	CAGGCAATTA	TAGAAATCAA	TGGGAAAATT	ATTTCTAATA	AAGGGAAAGA	2887
AAAGCAAGTT	GTCCATTTAG	AAAAAGGAAA	ATTAGTTCCA	ATCAAAATAG	AGTATCAATC	2947
AGATACAAAA	TTTAATATTG	ACAGTAAAAC	ATTTAAAGAA	CTTAAATTAT	TTAAAATAGA	3007
TAGTCAAAAC	CAACCCAGC	AAGTCCAGCA	AGATGAACTG	AGAAATCCTG	AATTTAACAA	3067
GAAAGAATCA	CAGGAATTCT	TAGCGAAACC	ATCGAAAATA	AATCTTTTCA	CTCAAAAAAT	3127
GAAAAGGGAA	ATTGATGAAG	ACACGGATAC	GGATGGGGAC	TCTATTCTCTG	ACCTTTGGGA	3187
AGAAAATGGG	TATACGATTC	ACAATAGAAT	CGCTGTAAAG	TGGGACGATT	CTCTAGCAAG	3247
TAAAGGGTAT	ACGAAATTTG	TTTCAAATCC	ACTAGAAAGT	CACACAGTTG	GTGATCCTTA	3307
TACAGATTAT	GAAAAGGCAG	CAAGAGATCT	AGATTTGTCA	AATGCAAAGG	AAACGTTTAA	3367
CCCATTGGTA	GCTGCTTTTC	CAAGTGTGAA	TGTTAGTATG	GAAAAGGTGA	TATTATCACC	3427
AAATGAAAAT	TTATCCAATA	GTGTAGAGTC	TCATTCATCC	ACGAATTGGT	CTTATACAAA	3487
TACAGAAGGT	GCTTCTGTTG	AAGCGGGGAT	TGGACCAAAA	GGTATTTCTG	TCGGAGTTAG	3547
CGTAAACTAT	CAACACTCTG	AAACAGTTGC	ACAAGAATGG	GGAACATCTA	CAGGAAATAC	3607
TTCGCAATTC	AATACGGCTT	CAGCGGGATA	TTTAAATGCA	AATGTTTCGAT	ATAACAATGT	3667
AGGAACTGGT	GCCATCTACG	ATGTAAAACC	TACAACAAGT	TTTGTATTAA	ATAACGATAC	3727
TATCGCAACT	ATTACGGCGA	AATCTAATTC	TACAGCCTTA	AATATATCTC	CTGGAGAAAG	3787
TTACCCGAAA	AAAGGACAAA	ATGGAATCGC	AATAACATCA	ATGGATGATT	TTAATTCCCA	3847
TCCGATTACA	TTAAATAAAA	AACAAGTAGA	TAATCTGCTA	AATAATAAAC	CTATGATGTT	3907
GGAAACAAAC	CAACAGATG	GTGTTTATAA	GATAAAAGAT	ACACATGGAA	ATATAGTAAC	3967
TGGCGGAGAA	TGGAATGGTG	TCATACAACA	AATCAAGGCT	AAAACAGCGT	CTATTATTGT	4027
GGATGATGGG	GAACGTGTAG	CAGAAAAACG	TGTAGCGGCA	AAAGATTATG	AAAATCCAGA	4087
AGATAAAACA	CCGTCTTTAA	CTTTAAAGA	TGCCCTGAAG	CTTTCATATC	CAGATGAAAT	4147
AAAAGAAATA	GAGGGATTAT	TATATTATAA	AAACAAACCG	ATATACGAAT	CGAGCGTTAT	4207
GACTTACTTA	GATGAAAATA	CAGCAAAAGA	AGTGACCAAA	CAATTAAATG	ATACCACTGG	4267
GAAATTTAAA	GATGTAAGTC	ATTTATATGA	TGTAAAACTG	ACTCCAAAAA	TGAATGTTAC	4327
AATCAAATTG	TCTATACTTT	ATGATAATGC	TGAGTCTAAT	GATAACTCAA	TTGGTAAATG	4387
GACAAACACA	AATATTGTTT	CAGGTGGAAA	TAACGGAAAA	AAACAATATT	CTTCTAATAA	4447

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TCCGGATGCT AATTTGACAT TAAATACAGA TGCTCAAGAA AAATTAAATA AAAATCGTGA	4507
CTATTATATA AGTTTATATA TGAAGTCAGA AAAAAACACA CAATGTGAGA TTACTATAGA	4567
TGGGGAGATT TATCCGATCA CTACAAAAAC AGTGAATGTG AATAAAGACA ATTACAAAAG	4627
ATTAGATATT ATAGCTCATA ATATAAAAAG TAATCCAATT TCTTCACTTC ATATTAAAAC	4687
GAATGATGAA ATAACTTTAT TTTGGGATGA TATTTCTATA ACAGATGTAG CATCAATAAA	4747
ACCGGAAAAT TTAACAGATT CAGAAATTAA ACAGATTTAT AGTAGGTATG GTATTAAAGTT	4807
AGAAGATGGA ATCCTTATTG ATAAAAAAGG TGGGATTCAT TATGGTGAAT TTATTAATGA	4867
AGCTAGTTTT AATATTGAAC CATTGCAAAA TTATGTGACC AAATATGAAG TTACTTATAG	4927
TAGTGAGTTA GGACCAAACG TGAGTGACAC ACTTGAAAGT GATAAAATTT ACAAGGATGG	4987
GACAATTAAA TTTGATTTTA CCAAATATAG TAAAAATGAA CAAGGATTAT TTTATGACAG	5047
TGGATTAAAT TGGGACTTTA AAATTAATGC TATTACTTAT GATGGTAAAG AGATGAATGT	5107
TTTTCATAGA TATAATAAAT AGTTATTATA TCTATGAAGC TGGTGCTAAA GATAGTGTA	5167
AAGTTAATAT ACTGTAGGAT TGTAATAAAA GTAATGGAAT TGATATCGTA CTTTGGAGTG	5227
GGGGATACTT TGTAATAGT TCTATCAGAA ACATTAGACT AAGAAAAGTT ACTACCCCCA	5287
CTTGAAAATG AAGATTCAAC TGATTACAAA CAACCTGTTA AATATTATAA GGTMTTAACA	5347
AAATATTAAA CTCMTTATGT TAATACTGTA ATATAAAGAG TTTAATTGTA TTCAAATGAA	5407
GCTTCCCAC AAAATTAGAC TGATTATCTA ATGAAATAAT CAGTCTAATT TTGTAGAACA	5467
GGTCTGGTAT TATTGTACGT GGTCACTAAA AGATATCTAA TATTATTGGG CAAGGCGTTC	5527
CATGATTGAA TCCTCGAATG TCTTGCCCTT TTCATTTATT TAAGAAGGAT TGTGGAGAAA	5587
TTATGGTTTA GATAATGAAG AAAGACTTCA CTTCTAATTT TTGATGTAA ATAAATCAAA	5647
ATTTGGCGAT TCACATTGTT TAATCCACTG ATAAAACATA CTGGAGTGTT CTTAAAAAAT	5707
CAGCTTTTTT CTTTATAAAA TTTTGCTTAG CGTACGAAAT TCGTGTTTTG TTGGTGGGAC	5767
CCCATGCCCA TCAACTTAAG AGTAAATTAG TAATGAACTT TCGTTCATCT GGATTAAAAT	5827
AACCTCAAAT TAGGACATGT TTTTAAAAAT AAGCAGACCA AATAAGCCTA GAATAGGTAT	5887
CATTTTTAAA AATTATGCTG CTTTCTTTTG TTTTCCAAAT CCATTATACT CATAAGCAAC	5947
ACCCATAATG TCAAAGACTG TTTTGTCTC ATATCGATAA GCTTGATATC GAATTCCTGC	6007
AGCCCGGGGG ATCCACTAGT TCTAGAGCGG CCGCCACCGC GG	6049

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Lys Arg Met Glu Gly Lys Leu Phe Met Val Ser Lys Lys Leu Gln
 1             5             10             15

Val Val Thr Lys Thr Val Leu Leu Ser Thr Val Phe Ser Ile Ser Leu
      20             25             30

Leu Asn Asn Glu Val Ile Lys Ala Glu Gln Leu Asn Ile Asn Ser Gln
      35             40             45

Ser Lys Tyr Thr Asn Leu Gln Asn Leu Lys Ile Thr Asp Lys Val Glu
 50             55             60

Asp Phe Lys Glu Asp Lys Glu Lys Ala Lys Glu Trp Gly Lys Glu Lys
 65             70             75             80

Glu Lys Glu Trp Lys Leu Thr Ala Thr Glu Lys Gly Lys Met Asn Asn
      85             90             95

Phe Leu Asp Asn Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr
      100             105             110

Phe Ser Met Ala Gly Ser Phe Glu Asp Glu Ile Lys Asp Leu Lys Glu
      115             120             125

Ile Asp Lys Met Phe Asp Lys Thr Asn Leu Ser Asn Ser Ile Ile Thr
      130             135             140

Tyr Lys Asn Val Glu Pro Thr Thr Ile Gly Phe Asn Lys Ser Leu Thr
      145             150             155             160

Glu Gly Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln
      165             170             175

Phe Leu Asp Arg Asp Ile Lys Phe Asp Ser Tyr Leu Asp Thr His Leu
      180             185             190

Thr Ala Gln Gln Val Ser Ser Lys Glu Arg Val Ile Leu Lys Val Thr
      195             200             205

Val Pro Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile
      210             215             220

Leu Asn Asn Ser Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Met Val
      225             230             235             240

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His Val Asp Lys Val Ser Lys Val Val Lys Lys Gly Val Glu Cys Leu
 245 250 255
 Gln Ile Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile
 260 265 270
 Asn Ala Glu Ala His Ser Trp Gly Met Lys Asn Tyr Glu Glu Trp Ala
 275 280 285
 Lys Asp Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg
 290 295 300
 Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser
 305 310 315 320
 Gly Asn Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala Leu
 325 330 335
 Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly
 340 345 350
 Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys
 355 360 365
 Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr
 370 375 380
 Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg
 385 390 395 400
 Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr
 405 410 415
 Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp
 420 425 430
 Lys Asp Ser Lys Tyr His Ile Asp Lys Val Thr Glu Val Ile Ile Lys
 435 440 445
 Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn
 450 455 460

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

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(A) NAME/KEY: Peptide
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /note= "Signal peptide for vacuolar targetting"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Ser Ser Ser Phe Ala Asp Ser Asn Pro Ile Arg Val Thr Asp Arg
 1 5 10 15
 Ala Ala Ser Thr
 20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2655 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Bacillus cereus
 (B) STRAIN: AB78
 (C) INDIVIDUAL ISOLATE: NRRL B-21058

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..2652
 (D) OTHER INFORMATION: /product= "100 kDa protein VIPIA(a)"
 /note= "This sequence is identical to the portion of SEQ ID NO:1 between and including nucleotide 2475 to 5126."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG AAA AAT ATG AAG AAA AAG TTA GCA AGT GTT GTA ACG TGT ACG TTA	48
Met Lys Asn Met Lys Lys Lys Leu Ala Ser Val Val Thr Cys Thr Leu	
465 470 475	
TTA GCT CCT ATG TTT TTG AAT GGA AAT GTG AAT GCT GTT TAC GCA GAC	96
Leu Ala Pro Met Phe Leu Asn Gly Asn Val Asn Ala Val Tyr Ala Asp	
480 485 490	
AGC AAA ACA AAT CAA ATT TCT ACA ACA CAG AAA AAT CAA CAG AAA GAG	144
Ser Lys Thr Asn Gln Ile Ser Thr Thr Gln Lys Asn Gln Gln Lys Glu	
495 500 505 510	

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ATG GAC CGA AAA GGA TTA CTT GGG TAT TAT TTC AAA GGA AAA GAT TTT Met Asp Arg Lys Gly Leu Leu Gly Tyr Tyr Phe Lys Gly Lys Asp Phe 515 520 525	192
AGT AAT CTT ACT ATG TTT GCA CCG ACA CGT GAT AGT ACT CTT ATT TAT Ser Asn Leu Thr Met Phe Ala Pro Thr Arg Asp Ser Thr Leu Ile Tyr 530 535 540	240
GAT CAA CAA ACA GCA AAT AAA CTA TTA GAT AAA AAA CAA CAA GAA TAT Asp Gln Gln Thr Ala Asn Lys Leu Leu Asp Lys Lys Gln Gln Glu Tyr 545 550 555	288
CAG TCT ATT CGT TGG ATT GGT TTG ATT CAG AGT AAA GAA ACG GGA GAT Gln Ser Ile Arg Trp Ile Gly Leu Ile Gln Ser Lys Glu Thr Gly Asp 560 565 570	336
TTC ACA TTT AAC TTA TCT GAG GAT GAA CAG GCA ATT ATA GAA ATC AAT Phe Thr Phe Asn Leu Ser Glu Asp Glu Gln Ala Ile Ile Glu Ile Asn 575 580 585 590	384
GGG AAA ATT ATT TCT AAT AAA GGG AAA GAA AAG CAA GTT GTC CAT TTA Gly Lys Ile Ile Ser Asn Lys Gly Lys Glu Lys Gln Val Val His Leu 595 600 605	432
GAA AAA GGA AAA TTA GTT CCA ATC AAA ATA GAG TAT CAA TCA GAT ACA Glu Lys Gly Lys Leu Val Pro Ile Lys Ile Glu Tyr Gln Ser Asp Thr 610 615 620	480
AAA TTT AAT ATT GAC AGT AAA ACA TTT AAA GAA CTT AAA TTA TTT AAA Lys Phe Asn Ile Asp Ser Lys Thr Phe Lys Glu Leu Lys Leu Phe Lys 625 630 635	528
ATA GAT AGT CAA AAC CAA CCC CAG CAA GTC CAG CAA GAT GAA CTG AGA Ile Asp Ser Gln Asn Gln Pro Gln Gln Val Gln Gln Asp Glu Leu Arg 640 645 650	576
AAT CCT GAA TTT AAC AAG AAA GAA TCA CAG GAA TTC TTA GCG AAA CCA Asn Pro Glu Phe Asn Lys Lys Glu Ser Gln Glu Phe Leu Ala Lys Pro 655 660 665 670	624
TCG AAA ATA AAT CTT TTC ACT CAA AAA ATG AAA AGG GAA ATT GAT GAA Ser Lys Ile Asn Leu Phe Thr Gln Lys Met Lys Arg Glu Ile Asp Glu 675 680 685	672
GAC ACG GAT ACG GAT GGG GAC TCT ATT CCT GAC CTT TGG GAA GAA AAT Asp Thr Asp Thr Asp Gly Asp Ser Ile Pro Asp Leu Trp Glu Glu Asn 690 695 700	720
GGG TAT ACG ATT CAA AAT AGA ATC GCT GTA AAG TGG GAC GAT TCT CTA Gly Tyr Thr Ile Gln Asn Arg Ile Ala Val Lys Trp Asp Asp Ser Leu 705 710 715	768
GCA AGT AAA GGG TAT ACG AAA TTT GTT TCA AAT CCA CTA GAA AGT CAC Ala Ser Lys Gly Tyr Thr Lys Phe Val Ser Asn Pro Leu Glu Ser His 720 725 730	816

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ACA GTT GGT GAT CCT TAT ACA GAT TAT GAA AAG GCA GCA AGA GAT CTA Thr Val Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ala Arg Asp Leu 735 740 745 750	864
GAT TTG TCA AAT GCA AAG GAA ACG TTT AAC CCA TTG GTA GCT GCT TTT Asp Leu Ser Asn Ala Lys Glu Thr Phe Asn Pro Leu Val Ala Ala Phe 755 760 765	912
CCA AGT GTG AAT GTT AGT ATG GAA AAG GTG ATA TTA TCA CCA AAT GAA Pro Ser Val Asn Val Ser Met Glu Lys Val Ile Leu Ser Pro Asn Glu 770 775 780	960
AAT TTA TCC AAT AGT GTA GAG TCT CAT TCA TCC ACG AAT TGG TCT TAT Asn Leu Ser Asn Ser Val Glu Ser His Ser Ser Thr Asn Trp Ser Tyr 785 790 795	1008
ACA AAT ACA GAA GGT GCT TCT GTT GAA GCG GGG ATT GGA CCA AAA GGT Thr Asn Thr Glu Gly Ala Ser Val Glu Ala Gly Ile Gly Pro Lys Gly 800 805 810	1056
ATT TCG TTC GGA GTT AGC GTA AAC TAT CAA CAC TCT GAA ACA GTT GCA Ile Ser Phe Gly Val Ser Val Asn Tyr Gln His Ser Glu Thr Val Ala 815 820 825 830	1104
CAA GAA TGG GGA ACA TCT ACA GGA AAT ACT TCG CAA TTC AAT ACG GCT Gln Glu Trp Gly Thr Ser Thr Gly Asn Thr Ser Gln Phe Asn Thr Ala 835 840 845	1152
TCA GCG GGA TAT TTA AAT GCA AAT GTT CGA TAT AAC AAT GTA GGA ACT Ser Ala Gly Tyr Leu Asn Ala Asn Val Arg Tyr Asn Asn Val Gly Thr 850 855 860	1200
GGT GCC ATC TAC GAT GTA AAA CCT ACA ACA AGT TTT GTA TTA AAT AAC Gly Ala Ile Tyr Asp Val Lys Pro Thr Thr Ser Phe Val Leu Asn Asn 865 870 875	1248
GAT ACT ATC GCA ACT ATT ACG GCG AAA TCT AAT TCT ACA GCC TTA AAT Asp Thr Ile Ala Thr Ile Thr Ala Lys Ser Asn Ser Thr Ala Leu Asn 880 885 890	1296
ATA TCT CCT GGA GAA AGT TAC CCG AAA AAA GGA CAA AAT GGA ATC GCA Ile Ser Pro Gly Glu Ser Tyr Pro Lys Lys Gly Gln Asn Gly Ile Ala 895 900 905 910	1344
ATA ACA TCA ATG GAT GAT TTT AAT TCC CAT CCG ATT ACA TTA AAT AAA Ile Thr Ser Met Asp Asp Phe Asn Ser His Pro Ile Thr Leu Asn Lys 915 920 925	1392
AAA CAA GTA GAT AAT CTG CTA AAT AAT AAA CCT ATG ATG TTG GAA ACA Lys Gln Val Asp Asn Leu Leu Asn Asn Lys Pro Met Met Leu Glu Thr 930 935 940	1440
AAC CAA ACA GAT GGT GTT TAT AAG ATA AAA GAT ACA CAT GGA AAT ATA Asn Gln Thr Asp Gly Val Tyr Lys Ile Lys Asp Thr His Gly Asn Ile	1488

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945	950	955	
GTA ACT GGC GGA GAA TGG AAT GGT GTC ATA CAA CAA ATC AAG GCT AAA Val Thr Gly Gly Glu Trp Asn Gly Val Ile Gln Gln Ile Lys Ala Lys 960 965 970	1536		
ACA GCG TCT ATT ATT GTG GAT GAT GGG GAA CGT GTA GCA GAA AAA CGT Thr Ala Ser Ile Ile Val Asp Asp Gly Glu Arg Val Ala Glu Lys Arg 975 980 985 990	1584		
GTA GCG GCA AAA GAT TAT GAA AAT CCA GAA GAT AAA ACA CCG TCT TTA Val Ala Ala Lys Asp Tyr Glu Asn Pro Glu Asp Lys Thr Pro Ser Leu 995 1000 1005	1632		
ACT TTA AAA GAT GCC CTG AAG CTT TCA TAT CCA GAT GAA ATA AAA GAA Thr Leu Lys Asp Ala Leu Lys Leu Ser Tyr Pro Asp Glu Ile Lys Glu 1010 1015 1020	1680		
ATA GAG GGA TTA TTA TAT TAT AAA AAC AAA CCG ATA TAC GAA TCG AGC Ile Glu Gly Leu Leu Tyr Tyr Lys Asn Lys Pro Ile Tyr Glu Ser Ser 1025 1030 1035	1728		
GTT ATG ACT TAC TTA GAT GAA AAT ACA GCA AAA GAA GTG ACC AAA CAA Val Met Thr Tyr Leu Asp Glu Asn Thr Ala Lys Glu Val Thr Lys Gln 1040 1045 1050	1776		
TTA AAT GAT ACC ACT GGG AAA TTT AAA GAT GTA AGT CAT TTA TAT GAT Leu Asn Asp Thr Thr Gly Lys Phe Lys Asp Val Ser His Leu Tyr Asp 1055 1060 1065 1070	1824		
GTA AAA CTG ACT CCA AAA ATG AAT GTT ACA ATC AAA TTG TCT ATA CTT Val Lys Leu Thr Pro Lys Met Asn Val Thr Ile Lys Leu Ser Ile Leu 1075 1080 1085	1872		
TAT GAT AAT GCT GAG TCT AAT GAT AAC TCA ATT GGT AAA TGG ACA AAC Tyr Asp Asn Ala Glu Ser Asn Asp Asn Ser Ile Gly Lys Trp Thr Asn 1090 1095 1100	1920		
ACA AAT ATT GTT TCA GGT GGA AAT AAC GGA AAA AAA CAA TAT TCT TCT Thr Asn Ile Val Ser Gly Gly Asn Asn Gly Lys Lys Gln Tyr Ser Ser 1105 1110 1115	1968		
AAT AAT CCG GAT GCT AAT TTG ACA TTA AAT ACA GAT GCT CAA GAA AAA Asn Asn Pro Asp Ala Asn Leu Thr Leu Asn Thr Asp Ala Gln Glu Lys 1120 1125 1130	2016		
TTA AAT AAA AAT CGT GAC TAT TAT ATA AGT TTA TAT ATG AAG TCA GAA Leu Asn Lys Asn Arg Asp Tyr Tyr Ile Ser Leu Tyr Met Lys Ser Glu 1135 1140 1145 1150	2064		
AAA AAC ACA CAA TGT GAG ATT ACT ATA GAT GGG GAG ATT TAT CCG ATC Lys Asn Thr Gln Cys Glu Ile Thr Ile Asp Gly Glu Ile Tyr Pro Ile 1155 1160 1165	2112		
ACT ACA AAA ACA GTG AAT GTG AAT AAA GAC AAT TAC AAA AGA TTA GAT	2160		

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Thr Thr Lys Thr Val Asn Val Asn Lys Asp Asn Tyr Lys Arg Leu Asp	
1170 1175 1180	
ATT ATA GCT CAT AAT ATA AAA AGT AAT CCA ATT TCT TCA CTT CAT ATT	2208
Ile Ile Ala His Asn Ile Lys Ser Asn Pro Ile Ser Ser Leu His Ile	
1185 1190 1195	
AAA ACG AAT GAT GAA ATA ACT TTA TTT TGG GAT GAT ATT TCT ATA ACA	2256
Lys Thr Asn Asp Glu Ile Thr Leu Phe Trp Asp Asp Ile Ser Ile Thr	
1200 1205 1210	
GAT GTA GCA TCA ATA AAA CCG GAA AAT TTA ACA GAT TCA GAA ATT AAA	2304
Asp Val Ala Ser Ile Lys Pro Glu Asn Leu Thr Asp Ser Glu Ile Lys	
1215 1220 1225 1230	
CAG ATT TAT AGT AGG TAT GGT ATT AAG TTA GAA GAT GGA ATC CTT ATT	2352
Gln Ile Tyr Ser Arg Tyr Gly Ile Lys Leu Glu Asp Gly Ile Leu Ile	
1235 1240 1245	
GAT AAA AAA GGT GGG ATT CAT TAT GGT GAA TTT ATT AAT GAA GCT AGT	2400
Asp Lys Lys Gly Gly Ile His Tyr Gly Glu Phe Ile Asn Glu Ala Ser	
1250 1255 1260	
TTT AAT ATT GAA CCA TTG CAA AAT TAT GTG ACC AAA TAT GAA GTT ACT	2448
Phe Asn Ile Glu Pro Leu Gln Asn Tyr Val Thr Lys Tyr Glu Val Thr	
1265 1270 1275	
TAT AGT AGT GAG TTA GGA CCA AAC GTG AGT GAC ACA CTT GAA AGT GAT	2496
Tyr Ser Ser Glu Leu Gly Pro Asn Val Ser Asp Thr Leu Glu Ser Asp	
1280 1285 1290	
AAA ATT TAC AAG GAT GGG ACA ATT AAA TTT GAT TTT ACC AAA TAT AGT	2544
Lys Ile Tyr Lys Asp Gly Thr Ile Lys Phe Asp Phe Thr Lys Tyr Ser	
1295 1300 1305 1310	
AAA AAT GAA CAA GGA TTA TTT TAT GAC AGT GGA TTA AAT TGG GAC TTT	2592
Lys Asn Glu Gln Gly Leu Phe Tyr Asp Ser Gly Leu Asn Trp Asp Phe	
1315 1320 1325	
AAA ATT AAT GCT ATT ACT TAT GAT GGT AAA GAG ATG AAT GTT TTT CAT	2640
Lys Ile Asn Ala Ile Thr Tyr Asp Gly Lys Glu Met Asn Val Phe His	
1330 1335 1340	
AGA TAT AAT AAA TAG	2655
Arg Tyr Asn Lys	
1345	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Lys Asn Met Lys Lys Lys Leu Ala Ser Val Val Thr Cys Thr Leu
 1           5           10           15
Leu Ala Pro Met Phe Leu Asn Gly Asn Val Asn Ala Val Tyr Ala Asp
          20           25           30
Ser Lys Thr Asn Gln Ile Ser Thr Thr Gln Lys Asn Gln Gln Lys Glu
          35           40           45
Met Asp Arg Lys Gly Leu Leu Gly Tyr Tyr Phe Lys Gly Lys Asp Phe
          50           55           60
Ser Asn Leu Thr Met Phe Ala Pro Thr Arg Asp Ser Thr Leu Ile Tyr
          65           70           75           80
Asp Gln Gln Thr Ala Asn Lys Leu Leu Asp Lys Lys Gln Gln Glu Tyr
          85           90           95
Gln Ser Ile Arg Trp Ile Gly Leu Ile Gln Ser Lys Glu Thr Gly Asp
          100          105          110
Phe Thr Phe Asn Leu Ser Glu Asp Glu Gln Ala Ile Ile Glu Ile Asn
          115          120          125
Gly Lys Ile Ile Ser Asn Lys Gly Lys Glu Lys Gln Val Val His Leu
          130          135          140
Glu Lys Gly Lys Leu Val Pro Ile Lys Ile Glu Tyr Gln Ser Asp Thr
          145          150          155          160
Lys Phe Asn Ile Asp Ser Lys Thr Phe Lys Glu Leu Lys Leu Phe Lys
          165          170          175
Ile Asp Ser Gln Asn Gln Pro Gln Gln Val Gln Gln Asp Glu Leu Arg
          180          185          190
Asn Pro Glu Phe Asn Lys Lys Glu Ser Gln Glu Phe Leu Ala Lys Pro
          195          200          205
Ser Lys Ile Asn Leu Phe Thr Gln Lys Met Lys Arg Glu Ile Asp Glu
          210          215          220
Asp Thr Asp Thr Asp Gly Asp Ser Ile Pro Asp Leu Trp Glu Glu Asn
          225          230          235          240
Gly Tyr Thr Ile Gln Asn Arg Ile Ala Val Lys Trp Asp Asp Ser Leu
          245          250          255
Ala Ser Lys Gly Tyr Thr Lys Phe Val Ser Asn Pro Leu Glu Ser His
          260          265          270

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Thr Val Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ala Arg Asp Leu
 275 280 285
 Asp Leu Ser Asn Ala Lys Glu Thr Phe Asn Pro Leu Val Ala Ala Phe
 290 295 300
 Pro Ser Val Asn Val Ser Met Glu Lys Val Ile Leu Ser Pro Asn Glu
 305 310 315 320
 Asn Leu Ser Asn Ser Val Glu Ser His Ser Ser Thr Asn Trp Ser Tyr
 325 330 335
 Thr Asn Thr Glu Gly Ala Ser Val Glu Ala Gly Ile Gly Pro Lys Gly
 340 345 350
 Ile Ser Phe Gly Val Ser Val Asn Tyr Gln His Ser Glu Thr Val Ala
 355 360 365
 Gln Glu Trp Gly Thr Ser Thr Gly Asn Thr Ser Gln Phe Asn Thr Ala
 370 375 380
 Ser Ala Gly Tyr Leu Asn Ala Asn Val Arg Tyr Asn Asn Val Gly Thr
 385 390 395 400
 Gly Ala Ile Tyr Asp Val Lys Pro Thr Thr Ser Phe Val Leu Asn Asn
 405 410 415
 Asp Thr Ile Ala Thr Ile Thr Ala Lys Ser Asn Ser Thr Ala Leu Asn
 420 425 430
 Ile Ser Pro Gly Glu Ser Tyr Pro Lys Lys Gly Gln Asn Gly Ile Ala
 435 440 445
 Ile Thr Ser Met Asp Asp Phe Asn Ser His Pro Ile Thr Leu Asn Lys
 450 455 460
 Lys Gln Val Asp Asn Leu Leu Asn Asn Lys Pro Met Met Leu Glu Thr
 465 470 475 480
 Asn Gln Thr Asp Gly Val Tyr Lys Ile Lys Asp Thr His Gly Asn Ile
 485 490 495
 Val Thr Gly Gly Glu Trp Asn Gly Val Ile Gln Gln Ile Lys Ala Lys
 500 505 510
 Thr Ala Ser Ile Ile Val Asp Asp Gly Glu Arg Val Ala Glu Lys Arg
 515 520 525
 Val Ala Ala Lys Asp Tyr Glu Asn Pro Glu Asp Lys Thr Pro Ser Leu
 530 535 540
 Thr Leu Lys Asp Ala Leu Lys Leu Ser Tyr Pro Asp Glu Ile Lys Glu
 545 550 555 560
 Ile Glu Gly Leu Leu Tyr Tyr Lys Asn Lys Pro Ile Tyr Glu Ser Ser

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565	570	575
Val Met Thr Tyr 580	Leu Asp Glu Asn Thr 585	Ala Lys Glu Val Thr Lys Gln 590
Leu Asn Asp Thr Thr Gly Lys Phe 595	Lys Asp Val Ser His 600	Leu Tyr Asp 605
Val Lys Leu Thr Pro Lys Met Asn Val Thr Ile Lys Leu Ser Ile Leu 610	615	620
Tyr Asp Asn Ala Glu Ser Asn Asp Asn Ser Ile Gly Lys Trp Thr Asn 625	630	635
Thr Asn Ile Val Ser Gly Gly Asn Asn Gly Lys Lys Gln Tyr Ser Ser 645	650	655
Asn Asn Pro Asp Ala Asn Leu Thr Leu Asn Thr Asp Ala Gln Glu Lys 660	665	670
Leu Asn Lys Asn Arg Asp Tyr Tyr Ile Ser Leu Tyr Met Lys Ser Glu 675	680	685
Lys Asn Thr Gln Cys Glu Ile Thr Ile Asp Gly Glu Ile Tyr Pro Ile 690	695	700
Thr Thr Lys Thr Val Asn Val Asn Lys Asp Asn Tyr Lys Arg Leu Asp 705	710	715
Ile Ile Ala His Asn Ile Lys Ser Asn Pro Ile Ser Ser Leu His Ile 725	730	735
Lys Thr Asn Asp Glu Ile Thr Leu Phe Trp Asp Asp Ile Ser Ile Thr 740	745	750
Asp Val Ala Ser Ile Lys Pro Glu Asn Leu Thr Asp Ser Glu Ile Lys 755	760	765
Gln Ile Tyr Ser Arg Tyr Gly Ile Lys Leu Glu Asp Gly Ile Leu Ile 770	775	780
Asp Lys Lys Gly Gly Ile His Tyr Gly Glu Phe Ile Asn Glu Ala Ser 785	790	795
Phe Asn Ile Glu Pro Leu Gln Asn Tyr Val Thr Lys Tyr Glu Val Thr 805	810	815
Tyr Ser Ser Glu Leu Gly Pro Asn Val Ser Asp Thr Leu Glu Ser Asp 820	825	830
Lys Ile Tyr Lys Asp Gly Thr Ile Lys Phe Asp Phe Thr Lys Tyr Ser 835	840	845
Lys Asn Glu Gln Gly Leu Phe Tyr Asp Ser Gly Leu Asn Trp Asp Phe 850	855	860

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Lys Ile Asn Ala Ile Thr Tyr Asp Gly Lys Glu Met Asn Val Phe His
 865 870 875 880

Arg Tyr Asn Lys

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2004 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: AB78
- (C) INDIVIDUAL ISOLATE: NRRL B-21058

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2001
- (D) OTHER INFORMATION: /product= "80 kDa protein VIP1A(a)"

/note= "This sequence is identical to that found in SEQ ID NO:1
 between and including nucleotide positions 3126 and 5126"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG AAA AGG GAA ATT GAT GAA GAC ACG GAT ACG GAT GGG GAC TCT ATT	48
Met Lys Arg Glu Ile Asp Glu Asp Thr Asp Thr Asp Gly Asp Ser Ile	
885 890 895 900	
CCT GAC CTT TGG GAA GAA AAT GGG TAT ACG ATT CAA AAT AGA ATC GCT	96
Pro Asp Leu Trp Glu Glu Asn Gly Tyr Thr Ile Gln Asn Arg Ile Ala	
905 910 915	
GTA AAG TGG GAC GAT TCT CTA GCA AGT AAA GGG TAT ACG AAA TTT GTT	144
Val Lys Trp Asp Asp Ser Leu Ala Ser Lys Gly Tyr Thr Lys Phe Val	
920 925 930	
TCA AAT CCA CTA GAA AGT CAC ACA GTT GGT GAT CCT TAT ACA GAT TAT	192
Ser Asn Pro Leu Glu Ser His Thr Val Gly Asp Pro Tyr Thr Asp Tyr	
935 940 945	
GAA AAG GCA GCA AGA GAT CTA GAT TTG TCA AAT GCA AAG GAA ACG TTT	240
Glu Lys Ala Ala Arg Asp Leu Asp Leu Ser Asn Ala Lys Glu Thr Phe	
950 955 960	

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AAC CCA TTG GTA GCT GCT TTT CCA AGT GTG AAT GTT AGT ATG GAA AAG Asn Pro Leu Val Ala Ala Phe Pro Ser Val Asn Val Ser Met Glu Lys 965 970 975 980	288
GTG ATA TTA TCA CCA AAT GAA AAT TTA TCC AAT AGT GTA GAG TCT CAT Val Ile Leu Ser Pro Asn Glu Asn Leu Ser Asn Ser Val Glu Ser His 985 990 995	336
TCA TCC ACG AAT TGG TCT TAT ACA AAT ACA GAA GGT GCT TCT GTT GAA Ser Ser Thr Asn Trp Ser Tyr Thr Asn Thr Glu Gly Ala Ser Val Glu 1000 1005 1010	384
GCG GGG ATT GGA CCA AAA GGT ATT TCG TTC GGA GTT AGC GTA AAC TAT Ala Gly Ile Gly Pro Lys Gly Ile Ser Phe Gly Val Ser Val Asn Tyr 1015 1020 1025	432
CAA CAC TCT GAA ACA GTT GCA CAA GAA TGG GGA ACA TCT ACA GGA AAT Gln His Ser Glu Thr Val Ala Gln Glu Trp Gly Thr Ser Thr Gly Asn 1030 1035 1040	480
ACT TCG CAA TTC AAT ACG GCT TCA GCG GGA TAT TTA AAT GCA AAT GTT Thr Ser Gln Phe Asn Thr Ala Ser Ala Gly Tyr Leu Asn Ala Asn Val 1045 1050 1055 1060	528
CGA TAT AAC AAT GTA GGA ACT GGT GCC ATC TAC GAT GTA AAA CCT ACA Arg Tyr Asn Asn Val Gly Thr Gly Ala Ile Tyr Asp Val Lys Pro Thr 1065 1070 1075	576
ACA AGT TTT GTA TTA AAT AAC GAT ACT ATC GCA ACT ATT ACG GCG AAA Thr Ser Phe Val Leu Asn Asn Asp Thr Ile Ala Thr Ile Thr Ala Lys 1080 1085 1090	624
TCT AAT TCT ACA GCC TTA AAT ATA TCT CCT GGA GAA AGT TAC CCG AAA Ser Asn Ser Thr Ala Leu Asn Ile Ser Pro Gly Glu Ser Tyr Pro Lys 1095 1100 1105	672
AAA GGA CAA AAT GGA ATC GCA ATA ACA TCA ATG GAT GAT TTT AAT TCC Lys Gly Gln Asn Gly Ile Ala Ile Thr Ser Met Asp Asp Phe Asn Ser 1110 1115 1120	720
CAT CCG ATT ACA TTA AAT AAA AAA CAA GTA GAT AAT CTG CTA AAT AAT His Pro Ile Thr Leu Asn Lys Lys Gln Val Asp Asn Leu Leu Asn Asn 1125 1130 1135 1140	768
AAA CCT ATG ATG TTG GAA ACA AAC CAA ACA GAT GGT GTT TAT AAG ATA Lys Pro Met Met Leu Glu Thr Asn Gln Thr Asp Gly Val Tyr Lys Ile 1145 1150 1155	816
AAA GAT ACA CAT GGA AAT ATA GTA ACT GGC GGA GAA TGG AAT GGT GTC Lys Asp Thr His Gly Asn Ile Val Thr Gly Gly Glu Trp Asn Gly Val 1160 1165 1170	864
ATA CAA CAA ATC AAG GCT AAA ACA GCG TCT ATT ATT GTG GAT GAT GGG Ile Gln Gln Ile Lys Ala Lys Thr Ala Ser Ile Ile Val Asp Asp Gly	912

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1175	1180	1185	
GAA CGT GTA GCA GAA AAA CGT GTA GCG GCA AAA GAT TAT GAA AAT CCA			960
Glu Arg Val Ala Glu Lys Arg Val Ala Ala Lys Asp Tyr Glu Asn Pro			
1190	1195	1200	
GAA GAT AAA ACA CCG TCT TTA ACT TTA AAA GAT GCC CTG AAG CTT TCA			1008
Glu Asp Lys Thr Pro Ser Leu Thr Leu Lys Asp Ala Leu Lys Leu Ser			
1205	1210	1215	1220
TAT CCA GAT GAA ATA AAA GAA ATA GAG GGA TTA TTA TAT TAT AAA AAC			1056
Tyr Pro Asp Glu Ile Lys Glu Ile Glu Gly Leu Leu Tyr Tyr Lys Asn			
1225	1230	1235	
AAA CCG ATA TAC GAA TCG AGC GTT ATG ACT TAC TTA GAT GAA AAT ACA			1104
Lys Pro Ile Tyr Glu Ser Ser Val Met Thr Tyr Leu Asp Glu Asn Thr			
1240	1245	1250	
GCA AAA GAA GTG ACC AAA CAA TTA AAT GAT ACC ACT GGG AAA TTT AAA			1152
Ala Lys Glu Val Thr Lys Gln Leu Asn Asp Thr Thr Gly Lys Phe Lys			
1255	1260	1265	
GAT GTA AGT CAT TTA TAT GAT GTA AAA CTG ACT CCA AAA ATG AAT GTT			1200
Asp Val Ser His Leu Tyr Asp Val Lys Leu Thr Pro Lys Met Asn Val			
1270	1275	1280	
ACA ATC AAA TTG TCT ATA CTT TAT GAT AAT GCT GAG TCT AAT GAT AAC			1248
Thr Ile Lys Leu Ser Ile Leu Tyr Asp Asn Ala Glu Ser Asn Asp Asn			
1285	1290	1295	1300
TCA ATT GGT AAA TGG ACA AAC ACA AAT ATT GTT TCA GGT GGA AAT AAC			1296
Ser Ile Gly Lys Trp Thr Asn Thr Asn Ile Val Ser Gly Gly Asn Asn			
1305	1310	1315	
GGA AAA AAA CAA TAT TCT TCT AAT AAT CCG GAT GCT AAT TTG ACA TTA			1344
Gly Lys Lys Gln Tyr Ser Ser Asn Asn Pro Asp Ala Asn Leu Thr Leu			
1320	1325	1330	
AAT ACA GAT GCT CAA GAA AAA TTA AAT AAA AAT CGT GAC TAT TAT ATA			1392
Asn Thr Asp Ala Gln Glu Lys Leu Asn Lys Asn Arg Asp Tyr Tyr Ile			
1335	1340	1345	
AGT TTA TAT ATG AAG TCA GAA AAA AAC ACA CAA TGT GAG ATT ACT ATA			1440
Ser Leu Tyr Met Lys Ser Glu Lys Asn Thr Gln Cys Glu Ile Thr Ile			
1350	1355	1360	
GAT GGG GAG ATT TAT CCG ATC ACT ACA AAA ACA GTG AAT GTG AAT AAA			1488
Asp Gly Glu Ile Tyr Pro Ile Thr Thr Lys Thr Val Asn Val Asn Lys			
1365	1370	1375	1380
GAC AAT TAC AAA AGA TTA GAT ATT ATA GCT CAT AAT ATA AAA AGT AAT			1536
Asp Asn Tyr Lys Arg Leu Asp Ile Ile Ala His Asn Ile Lys Ser Asn			
1385	1390	1395	
CCA ATT TCT TCA CTT CAT ATT AAA ACG AAT GAT GAA ATA ACT TTA TTT			1584

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Pro	Ile	Ser	Ser	Leu	His	Ile	Lys	Thr	Asn	Asp	Glu	Ile	Thr	Leu	Phe		
			1400					1405					1410				
TGG	GAT	GAT	ATT	TCT	ATA	ACA	GAT	GTA	GCA	TCA	ATA	AAA	CCG	GAA	AAT	1632	
Trp	Asp	Asp	Ile	Ser	Ile	Thr	Asp	Val	Ala	Ser	Ile	Lys	Pro	Glu	Asn		
			1415				1420					1425					
TTA	ACA	GAT	TCA	GAA	ATT	AAA	CAG	ATT	TAT	AGT	AGG	TAT	GGT	ATT	AAG	1680	
Leu	Thr	Asp	Ser	Glu	Ile	Lys	Gln	Ile	Tyr	Ser	Arg	Tyr	Gly	Ile	Lys		
			1430				1435				1440						
TTA	GAA	GAT	GGA	ATC	CTT	ATT	GAT	AAA	AAA	GGT	GGG	ATT	CAT	TAT	GGT	1728	
Leu	Glu	Asp	Gly	Ile	Leu	Ile	Asp	Lys	Lys	Gly	Gly	Ile	His	Tyr	Gly		
			1445				1450			1455					1460		
GAA	TTT	ATT	AAT	GAA	GCT	AGT	TTT	AAT	ATT	GAA	CCA	TTG	CCA	AAT	TAT	1776	
Glu	Phe	Ile	Asn	Glu	Ala	Ser	Phe	Asn	Ile	Glu	Pro	Leu	Pro	Asn	Tyr		
				1465				1470						1475			
GTG	ACC	AAA	TAT	GAA	GTT	ACT	TAT	AGT	AGT	GAG	TTA	GGA	CCA	AAC	GTG	1824	
Val	Thr	Lys	Tyr	Glu	Val	Thr	Tyr	Ser	Ser	Glu	Leu	Gly	Pro	Asn	Val		
			1480					1485					1490				
AGT	GAC	ACA	CTT	GAA	AGT	GAT	AAA	ATT	TAC	AAG	GAT	GGG	ACA	ATT	AAA	1872	
Ser	Asp	Thr	Leu	Glu	Ser	Asp	Lys	Ile	Tyr	Lys	Asp	Gly	Thr	Ile	Lys		
			1495				1500					1505					
TTT	GAT	TTT	ACC	AAA	TAT	AGT	AAA	AAT	GAA	CAA	GGA	TTA	TTT	TAT	GAC	1920	
Phe	Asp	Phe	Thr	Lys	Tyr	Ser	Lys	Asn	Glu	Gln	Gly	Leu	Phe	Tyr	Asp		
			1510				1515				1520						
AGT	GGA	TTA	AAT	TGG	GAC	TTT	AAA	ATT	AAT	GCT	ATT	ACT	TAT	GAT	GGT	1968	
Ser	Gly	Leu	Asn	Trp	Asp	Phe	Lys	Ile	Asn	Ala	Ile	Thr	Tyr	Asp	Gly		
			1525				1530			1535					1540		
AAA	GAG	ATG	AAT	GTT	TTT	CAT	AGA	TAT	AAT	AAA	TAG					2004	
Lys	Glu	Met	Asn	Val	Phe	His	Arg	Tyr	Asn	Lys							
				1545					1550								

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Lys	Arg	Glu	Ile	Asp	Glu	Asp	Thr	Asp	Thr	Asp	Gly	Asp	Ser	Ile
1				5				10						15	

Pro Asp Leu Trp Glu Glu Asn Gly Tyr Thr Ile Gln Asn Arg Ile Ala

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20	25	30
Val Lys Trp Asp Asp Ser Leu Ala Ser Lys Gly Tyr Thr Lys Phe Val		
35	40	45
Ser Asn Pro Leu Glu Ser His Thr Val Gly Asp Pro Tyr Thr Asp Tyr		
50	55	60
Glu Lys Ala Ala Arg Asp Leu Asp Leu Ser Asn Ala Lys Glu Thr Phe		
65	70	75
Asn Pro Leu Val Ala Ala Phe Pro Ser Val Asn Val Ser Met Glu Lys		
85	90	95
Val Ile Leu Ser Pro Asn Glu Asn Leu Ser Asn Ser Val Glu Ser His		
100	105	110
Ser Ser Thr Asn Trp Ser Tyr Thr Asn Thr Glu Gly Ala Ser Val Glu		
115	120	125
Ala Gly Ile Gly Pro Lys Gly Ile Ser Phe Gly Val Ser Val Asn Tyr		
130	135	140
Gln His Ser Glu Thr Val Ala Gln Glu Trp Gly Thr Ser Thr Gly Asn		
145	150	155
Thr Ser Gln Phe Asn Thr Ala Ser Ala Gly Tyr Leu Asn Ala Asn Val		
165	170	175
Arg Tyr Asn Asn Val Gly Thr Gly Ala Ile Tyr Asp Val Lys Pro Thr		
180	185	190
Thr Ser Phe Val Leu Asn Asn Asp Thr Ile Ala Thr Ile Thr Ala Lys		
195	200	205
Ser Asn Ser Thr Ala Leu Asn Ile Ser Pro Gly Glu Ser Tyr Pro Lys		
210	215	220
Lys Gly Gln Asn Gly Ile Ala Ile Thr Ser Met Asp Asp Phe Asn Ser		
225	230	235
His Pro Ile Thr Leu Asn Lys Lys Gln Val Asp Asn Leu Leu Asn Asn		
245	250	255
Lys Pro Met Met Leu Glu Thr Asn Gln Thr Asp Gly Val Tyr Lys Ile		
260	265	270
Lys Asp Thr His Gly Asn Ile Val Thr Gly Gly Glu Trp Asn Gly Val		
275	280	285
Ile Gln Gln Ile Lys Ala Lys Thr Ala Ser Ile Ile Val Asp Asp Gly		
290	295	300
Glu Arg Val Ala Glu Lys Arg Val Ala Ala Lys Asp Tyr Glu Asn Pro		
305	310	315
		320

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Glu Asp Lys Thr Pro Ser Leu Thr Leu Lys Asp Ala Leu Lys Leu Ser
 325 330 335
 Tyr Pro Asp Glu Ile Lys Glu Ile Glu Gly Leu Leu Tyr Tyr Lys Asn
 340 345 350
 Lys Pro Ile Tyr Glu Ser Ser Val Met Thr Tyr Leu Asp Glu Asn Thr
 355 360 365
 Ala Lys Glu Val Thr Lys Gln Leu Asn Asp Thr Thr Gly Lys Phe Lys
 370 375 380
 Asp Val Ser His Leu Tyr Asp Val Lys Leu Thr Pro Lys Met Asn Val
 385 390 395 400
 Thr Ile Lys Leu Ser Ile Leu Tyr Asp Asn Ala Glu Ser Asn Asp Asn
 405 410 415
 Ser Ile Gly Lys Trp Thr Asn Thr Asn Ile Val Ser Gly Gly Asn Asn
 420 425 430
 Gly Lys Lys Gln Tyr Ser Ser Asn Asn Pro Asp Ala Asn Leu Thr Leu
 435 440 445
 Asn Thr Asp Ala Gln Glu Lys Leu Asn Lys Asn Arg Asp Tyr Tyr Ile
 450 455 460
 Ser Leu Tyr Met Lys Ser Glu Lys Asn Thr Gln Cys Glu Ile Thr Ile
 465 470 475 480
 Asp Gly Glu Ile Tyr Pro Ile Thr Thr Lys Thr Val Asn Val Asn Lys
 485 490 495
 Asp Asn Tyr Lys Arg Leu Asp Ile Ile Ala His Asn Ile Lys Ser Asn
 500 505 510
 Pro Ile Ser Ser Leu His Ile Lys Thr Asn Asp Glu Ile Thr Leu Phe
 515 520 525
 Trp Asp Asp Ile Ser Ile Thr Asp Val Ala Ser Ile Lys Pro Glu Asn
 530 535 540
 Leu Thr Asp Ser Glu Ile Lys Gln Ile Tyr Ser Arg Tyr Gly Ile Lys
 545 550 555 560
 Leu Glu Asp Gly Ile Leu Ile Asp Lys Lys Gly Gly Ile His Tyr Gly
 565 570 575
 Glu Phe Ile Asn Glu Ala Ser Phe Asn Ile Glu Pro Leu Pro Asn Tyr
 580 585 590
 Val Thr Lys Tyr Glu Val Thr Tyr Ser Ser Glu Leu Gly Pro Asn Val
 595 600 605

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Ser Asp Thr Leu Glu Ser Asp Lys Ile Tyr Lys Asp Gly Thr Ile Lys
 610 615 620

Phe Asp Phe Thr Lys Tyr Ser Lys Asn Glu Gln Gly Leu Phe Tyr Asp
 625 630 635 640

Ser Gly Leu Asn Trp Asp Phe Lys Ile Asn Ala Ile Thr Tyr Asp Gly
 645 650 655

Lys Glu Met Asn Val Phe His Arg Tyr Asn Lys
 660 665

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Bacillus cereus
- (B) STRAIN: AB78
- (C) INDIVIDUAL ISOLATE: NRRL B-21058

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "N-terminal sequence of protein purified from strain AB78"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys Arg Glu Ile Asp Glu Asp Thr Asp Thr Asx Gly Asp Ser Ile Pro
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:9:

(i). SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1..21

(D) OTHER INFORMATION: /note= "Oligonucleotide probe based on amino acids 3 to 9 of SEQ ID NO:8, using codon usage of *Bacillus thuringiensis*"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAAATTGATC AAGATACNGA T

21

(2) INFORMATION FOR SEQ ID NO:10:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: AB88

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..14

(D) OTHER INFORMATION: /note= "N-terminal amino acid sequence of protein known as anion exchange fraction 23 (smaller)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Xaa Glu Pro Phe Val Ser Ala Xaa Xaa Xaa Gln Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: N-terminal

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Xaa	Glu	Tyr	Glu	Asn	Val	Glu	Pro	Phe	Val	Ser	Ala	Xaa
1				5					10			

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Asn	Lys	Asn	Asn	Thr	Lys	Leu	Pro	Thr	Arg	Ala	Leu	Pro
1				5					10				

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
- (B) STRAIN: AB88

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "N-terminal amino acid sequence of 35 kDa VIP active against *Agrotis ipsilon*"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala	Leu	Ser	Glu	Asn	Thr	Gly	Lys	Asp	Gly	Gly	Tyr	Ile	Val	Pro
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Asp	Asn	Asn	Pro	Asn	Ile	Asn	Glu
1				5				

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..9
- (D) OTHER INFORMATION: /note= "N-terminal sequence of 80 kDa delta-endotoxin"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Asp	Asn	Asn	Pro	Asn	Ile	Asn	Glu
1				5				

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids

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(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..11

(D) OTHER INFORMATION: /note= "N-terminal sequence from 60 kDa delta-endotoxin"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Asn	Val	Leu	Asn	Ser	Gly	Arg	Thr	Thr	Ile
1				5						10

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2655 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1..2652

(D) OTHER INFORMATION: /note= "Maize optimized DNA sequence for 100 kd VIP1A(a) protein from AB78"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGAAGAACA TGAAGAAGAA GCTGGCCAGC GTGGTGACCT GCACCCTGCT GGCCCCCATG	60
TTCTTGAACG GCAACGTGAA CGCCGTGTAC GCCGACAGCA AGACCAACCA GATCAGCACC	120
ACCCAGAAGA ACCAGCAGAA GGAGATGGAC CGCAAGGGCC TGCTGGGCTA CTACTTCAAG	180

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GGCAAGGACT TCAGCAACCT GACCATGTTC GCCCCACGC GTGACAGCAC CCTGATCTAC	240
GACCAGCAGA CCGCCAACAA GCTGCTGGAC AAGAAGCAGC AGGAGTACCA GAGCATCCGC	300
TGGATCGGCC TGATCCAGAG CAAGGAGACC GGCGACTTCA CCTTCAACCT GAGCGAGGAC	360
GAGCAGGCCA TCATCGAGAT CAACGGCAAG ATCATCAGCA ACAAGGGCAA GGAGAAGCAG	420
GTGGTGCACC TGGAGAAGGG CAAGCTGGTG CCCATCAAGA TCGAGTACCA GAGCGACACC	480
AAGTTCAACA TCGACAGCAA GACCTTCAAG GAGCTGAAGC TTTTCAAGAT CGACAGCCAG	540
AACCAGCCCC AGCAGGTGCA GCAGGACGAG CTGCGCAACC CCGAGTTCAA CAAGAAGGAG	600
AGCCAGGAGT TCCTGGCCAA GCCCAGCAAG ATCAACCTGT TCACCCAGCA GATGAAGCGC	660
GAGATCGACG AGGACACCGA CACCGACGGC GACAGCATCC CCGACCTGTG GGAGGAGAAC	720
GGCTACACCA TCCAGAACCG CATCGCCGTG AAGTGGGACG ACAGCCTGGC TAGCAAGGGC	780
TACACCAAGT TCGTGAGCAA CCCCCTGGAG AGCCACACCG TGGGCGACCC CTACACCGAC	840
TACGAGAAGG CCGCCCGGA CCTGGACCTG AGCAACGCCA AGGAGACCTT CAACCCCTG	900
GTGGCCGCCT TCCCCAGCGT GAACGTGAGC ATGGAGAAGG TGATCCTGAG CCCCAACGAG	960
AACCTGAGCA ACAGCGTGGA GAGCCACTCG AGCACCAACT GGAGCTACAC CAACACCGAG	1020
GGCGCCAGCG TGGAGGCCGG CATCGGTCCC AAGGGCATCA GCTTCGGCGT GAGCGTGAAC	1080
TACCAGCACA GCGAGACCGT GGCCCAGGAG TGGGGCACCA GCACCGGCAA CACCAGCCAG	1140
TTCAACACCG CCAGCGCCGG CTACCTGAAC GCCAACGTGC GCTACAACAA CGTGGGCACC	1200
GGCGCCATCT ACGAGTGAA GCCCACCACC AGCTTCGTGC TGAACAACGA CACCATCGCC	1260
ACCATCACCG CCAAGTCGAA TTCCACCGCC CTGAACATCA GCCCCGGCGA GAGCTACCCC	1320
AAGAAGGGCC AGAACGGCAT CGCCATCACC AGCATGGACG ACTTCAACAG CCACCCCATC	1380
ACCCTGAACA AGAAGCAGGT GGACAACCTG CTGAACAACA AGCCCATGAT GCTGGAGACC	1440
AACCAGACCG ACGGCGTCTA CAAGATCAAG GACACCCACG GCAACATCGT GACCGGCGGC	1500
GAGTGGAACG GCGTGATCCA GCAGATCAAG GCCAAGACCG CCAGCATCAT CGTCGACGAC	1560
GGCGAGCGCG TGGCCGAGAA GCGCGTGGCC GCCAAGGACT ACGAGAACCC CGAGGACAAG	1620
ACCCCCAGCC TGACCCTGAA GGACGCCCTG AAGCTGAGCT ACCCCGACGA GATCAAGGAG	1680
ATCGAGGGCC TGCTGTACTA CAAGAACAAG CCCATCTACG AGAGCAGCGT GATGACCTAT	1740
CTAGACGAGA ACACCGCCAA GGAGGTGACC AAGCAGCTGA ACGACACCAC CGGCAAGTTC	1800
AAGGACGTGA GCCACCTGTA CGACGTGAAG CTGACCCCCA AGATGAACGT GACCATCAAG	1860

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CTGAGCATCC TGTACGACAA CGCCGAGAGC AACGACAACA GCATCGGCAA GTGGACCAAC      1920
ACCAACATCG TGAGCGGCGG CAACAACGGC AAGAAGCAGT ACAGCAGCAA CAACCCCGAC      1980
GCCAACCTGA CCCTGAACAC CGACGCCCAG GAGAAGCTGA ACAAGAACCG CGACTACTAC      2040
ATCAGCCTGT ACATGAAGAG CGAGAAGAAC ACCCAGTGCG AGATCACCAT CGACGGCGAG      2100
ATATACCCCA TCACCACCAA GACCGTGAAC GTGAACAAGG ACAACTACAA GCGCCTGGAC      2160
ATCATCGCCC ACAACATCAA GAGCAACCCC ATCAGCAGCC TGCACATCAA GACCAAOGAC      2220
GAGATCACCC TGTTCCTGGA CGACATATCG ATTACCGACG TCGCCAGCAT CAAGCCCGAG      2280
AACCTGACCG ACAGCGAGAT CAAGCAGATA TACAGTCGCT ACGGCATCAA GCTGGAGGAC      2340
GGCATCCTGA TCGACAAGAA GGGCGGCATC CACTACGGCG AGTTCATCAA CGAGGCCAGC      2400
TTCAACATCG AGCCCCTGCA GAACTACGTG ACCAAGTACG AGGTGACCTA CAGCAGCGAG      2460
CTGGGCCCCA ACGTGAGCGA CACCCTGGAG AGCGACAAGA TTTACAAGGA CGGCACCATC      2520
AAGTTCGACT TCACCAAGTA CAGCAAGAAC GAGCAGGGCC TGTTCCTACG CAGCGGCCTG      2580
AACTGGGACT TCAAGATCAA CGCCATCACC TACGACGGCA AGGAGATGAA CGTGTTCAC      2640
CGCTACAACA AGTAG                                                    2655

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2004 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..2004
- (D) OTHER INFORMATION: /note= "Maize optimized DNA sequence for VIPlA(a) 80 kd protein from AB78"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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ATGAAGCGCG AGATCGACGA GGACACCGAC ACCGACGGCG ACAGCATCCC CGACCTGTGG      60

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GAGGAGAACG GCTACACCAT CCAGAACCGC ATCGCCGTGA AGTGGGACGA CAGCCTGGCT	120
AGCAAGGGCT ACACCAAGTT CGTGAGCAAC CCCCTGGAGA GCCACACCGT GGGCGACCCC	180
TACACCGACT ACGAGAAGGC CGCCCGCGAC CTGGACCTGA GCAACGCCAA GGAGACCTTC	240
AACCCCTGG TGGCCGCCTT CCCAGCGTG AACGTGAGCA TGGAGAAGGT GATCCTGAGC	300
CCCAACGAGA ACCTGAGCAA CAGCGTGGAG AGCCACTCGA GCACCAACTG GAGCTACACC	360
AACACCGAGG GCGCCAGCGT GGAGGCCGGC ATCGGTCCCA AGGGCATCAG CTTGGCGTG	420
AGCGTGAAGT ACCAGCACAG CGAGACCGTG GCCCAGGAGT GGGGCACCAG CACCGGCAAC	480
ACCAGCCAGT TCAACACCGC CAGCGCCGGC TACCTGAACG CCAACGTGCG CTACAACAAC	540
GTGGGCACCG GCGCCATCTA CGACGTGAAG CCCACCACCA GCTTCGTGCT GAACAACGAC	600
ACCATCGCCA CCATCACC GC CAAGTCGAAT TCCACCGCCC TGAACATCAG CCCCGGCGAG	660
AGCTACCCCA AGAAGGGCCA GAACGGCATC GCCATCACCA GCATGGACGA CTTCAACAGC	720
CACCCCATCA CCCTGAACAA GAAGCAGGTG GACAACCTGC TGAACAACAA GCCCATGATG	780
CTGGAGACCA ACCAGACCGA CGGCGTCTAC AAGATCAAGG ACACCCACGG CAACATCGTG	840
ACCGGCGGCG AGTGGAACGG CGTGATCCAG CAGATCAAGG CCAAGACCGC CAGCATCATC	900
GTCGACGACG GCGAGCGCGT GGCCGAGAAG CGCGTGGCCG CCAAGGACTA CGAGAACCCC	960
GAGGACAAGA CCCCAGCCT GACCCTGAAG GACGCCCTGA AGCTGAGCTA CCCCAGCAG	1020
ATCAAGGAGA TCGAGGGCCT GCTGTACTAC AAGAACAAGC CCATCTACGA GAGCAGCGTG	1080
ATGACCTATC TAGACGAGAA CACCGCCAAG GAGGTGACCA AGCAGCTGAA CGACACCACC	1140
GGCAAGTTCA AGGACGTGAG CCACCTGTAC GACGTGAAGC TGACCCCCAA GATGAACGTG	1200
ACCATCAAGC TGAGCATCCT GTACGACAAC GCCGAGAGCA ACGACAACAG CATCGGCAAG	1260
TGGACCAACA CCAACATCGT GAGCGGCGGC AACACGGCA AGAAGCAGTA CAGCAGCAAC	1320
AACCCGACG CCAACCTGAC CCTGAACACC GACGCCCAGG AGAAGCTGAA CAAGAACCGC	1380
GACTIONTACA TCAGCCTGTA CATGAAGAGC GAGAAGAACA CCCAGTGC GAATCACCATC	1440
GACGGCGAGA TATACCCCAT CACCACCAAG ACGTGAACG TGAACAAGGA CAACTACAAG	1500
CGCCTGGACA TCATCGCCCA CAACATCAAG AGCAACCCCA TCAGCAGCCT GCACATCAAG	1560
ACCAACGACG AGATCACCTT GTTCTGGGAC GACATATCGA TTACCGACGT CGCCAGCATC	1620
AAGCCCGAGA ACCTGACCGA CAGCGAGATC AAGCAGATAT ACAGTCGCTA CGGCATCAAG	1680
CTGGAGGACG GCATCCTGAT CGACAAGAAG GGCGGCATCC ACTACGGCGA GTTCATCAAC	1740

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GAGGCCAGCT TCAACATCGA GCCCCTGCAG AACTACGTGA CCAAGTACGA GGTGACCTAC 1800
 AGCAGCGAGC TGGGCCCCAA CGTGAGCGAC ACCCTGGAGA GCGACAAGAT TTACAAGGAC 1860
 GGCACCATCA AGTTCGACTT CACCAAGTAC AGCAAGAACG AGCAGGGCCT GTTCTACGAC 1920
 AGCGGCCTGA ACTGGGACTT CAAGATCAAC GCCATCACCT ACGACGGCAA GGAGATGAAC 1980
 GTGTTCCACC GCTACAACAA GTAG 2004

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1386
- (D) OTHER INFORMATION: /product= "VIP2A(b) from Btt"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1394..3895
- (D) OTHER INFORMATION: /product= "VIP1A(b) from Btt"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..4074
- (D) OTHER INFORMATION: /note= "Cloned DNA sequence from Btt which contains the genes for both VIP1A(b) and VIP2A(b) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG CAA AGA ATG GAG GGA AAG TTG TTT GTG GTG TCA AAA ACA TTA CAA 48
 Met Gln Arg Met Glu Gly Lys Leu Phe Val Val Ser Lys Thr Leu Gln
 670 675 680

GTA GTT ACT AGA ACT GTA TTG CTT AGT ACA GTT TAC TCT ATA ACT TTA 96
 Val Val Thr Arg Thr Val Leu Leu Ser Thr Val Tyr Ser Ile Thr Leu
 685 690 695

TTA AAT AAT GTA GTG ATA AAA GCT GAC CAA TTA AAT ATA AAT TCT CAA 144
 Leu Asn Asn Val Val Ile Lys Ala Asp Gln Leu Asn Ile Asn Ser Gln
 700 705 710 715

AGT AAA TAT ACT AAC TTG CAA AAT CTA AAA ATC CCT GAT AAT GCA GAG 192
 Ser Lys Tyr Thr Asn Leu Gln Asn Leu Lys Ile Pro Asp Asn Ala Glu

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720	725	730	
GAT TTT AAA GAA GAT AAG GGG AAA GCG AAA GAA TGG GGG AAA GAG AAA Asp Phe Lys Glu Asp Lys Gly Lys Ala Lys Glu Trp Gly Lys Glu Lys 735 740 745			240
GGG GAA GAG TGG AGG CCT CCT GCT ACT GAG AAA GGA GAA ATG AAT AAT Gly Glu Glu Trp Arg Pro Pro Ala Thr Glu Lys Gly Glu Met Asn Asn 750 755 760			288
TTT TTA GAT AAT AAA AAT GAT ATA AAG ACC AAT TAT AAA GAA ATT ACT Phe Leu Asp Asn Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr 765 770 775			336
TTT TCT ATG GCA GGT TCA TGT GAA GAT GAA ATA AAA GAT TTA GAA GAA Phe Ser Met Ala Gly Ser Cys Glu Asp Glu Ile Lys Asp Leu Glu Glu 780 785 790 795			384
ATT GAT AAG ATC TTT GAT AAA GCC AAT CTC TCG AGT TCT ATT ATC ACC Ile Asp Lys Ile Phe Asp Lys Ala Asn Leu Ser Ser Ser Ile Ile Thr 800 805 810			432
TAT AAA AAT GTG GAA CCA GCA ACA ATT GGA TTT AAT AAA TCT TTA ACA Tyr Lys Asn Val Glu Pro Ala Thr Ile Gly Phe Asn Lys Ser Leu Thr 815 820 825			480
GAA GGT AAT ACG ATT AAT TCT GAT GCA ATG GCA CAG TTT AAA GAA CAA Glu Gly Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln 830 835 840			528
TTT TTA GGT AAG GAT ATG AAG TTT GAT AGT TAT CTA GAT ACT CAT TTA Phe Leu Gly Lys Asp Met Lys Phe Asp Ser Tyr Leu Asp Thr His Leu 845 850 855			576
ACT GCT CAA CAA GTT TCC AGT AAA AAA AGA GTT ATT TTG AAG GTT ACG Thr Ala Gln Gln Val Ser Ser Lys Lys Arg Val Ile Leu Lys Val Thr 860 865 870 875			624
GTT CCG AGT GGG AAA GGT TCT ACT ACT CCA ACA AAA GCA GGT GTC ATT Val Pro Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile 880 885 890			672
TTA AAC AAT AAT GAA TAC AAA ATG CTC ATT GAT AAT GGG TAT GTG CTC Leu Asn Asn Asn Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Val Leu 895 900 905			720
CAT GTA GAT AAG GTA TCA AAA GTA GTA AAA AAA GGG ATG GAG TGC TTA His Val Asp Lys Val Ser Lys Val Val Lys Lys Gly Met Glu Cys Leu 910 915 920			768
CAA GTT GAA GGG ACT TTA AAA AAG AGT CTC GAC TTT AAA AAT GAT ATA Gln Val Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile 925 930 935			816
AAT GCT GAA GCG CAT AGC TGG GGG ATG AAA ATT TAT GAA GAC TGG GCT			864

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Asn	Ala	Glu	Ala	His	Ser	Trp	Gly	Met	Lys	Ile	Tyr	Glu	Asp	Trp	Ala	
940					945					950					955	
AAA	AAT	TTA	ACC	GCT	TCG	CAA	AGG	GAA	GCT	TTA	GAT	GGG	TAT	GCT	AGG	912
Lys	Asn	Leu	Thr	Ala	Ser	Gln	Arg	Glu	Ala	Leu	Asp	Gly	Tyr	Ala	Arg	
			960					965						970		
CAA	GAT	TAT	AAA	GAA	ATC	AAT	AAT	TAT	TTG	CGC	AAT	CAA	GGC	GGG	AGT	960
Gln	Asp	Tyr	Lys	Glu	Ile	Asn	Asn	Tyr	Leu	Arg	Asn	Gln	Gly	Gly	Ser	
			975					980						985		
GGA	AAT	GAA	AAG	CTG	GAT	GCC	CAA	TTA	AAA	AAT	ATT	TCT	GAT	GCT	TTA	1008
Gly	Asn	Glu	Lys	Leu	Asp	Ala	Gln	Leu	Lys	Asn	Ile	Ser	Asp	Ala	Leu	
		990					995					1000				
GGG	AAG	AAA	CCC	ATA	CCA	GAA	AAT	ATT	ACC	GTG	TAT	AGA	TGG	TGT	GGC	1056
Gly	Lys	Lys	Pro	Ile	Pro	Glu	Asn	Ile	Thr	Val	Tyr	Arg	Trp	Cys	Gly	
	1005					1010					1015					
ATG	CCG	GAA	TTT	GGT	TAT	CAA	ATT	AGT	GAT	CCG	TTA	CCT	TCT	TTA	AAA	1104
Met	Pro	Glu	Phe	Gly	Tyr	Gln	Ile	Ser	Asp	Pro	Leu	Pro	Ser	Leu	Lys	
1020				1025						1030					1035	
GAT	TTT	GAA	GAA	CAA	TTT	TTA	AAT	ACA	ATT	AAA	GAA	GAC	AAA	GGG	TAT	1152
Asp	Phe	Glu	Glu	Gln	Phe	Leu	Asn	Thr	Ile	Lys	Glu	Asp	Lys	Gly	Tyr	
				1040					1045					1050		
ATG	AGT	ACA	AGC	TTA	TCG	AGT	GAA	CGT	CTT	GCA	GCT	TTT	GGA	TCT	AGA	1200
Met	Ser	Thr	Ser	Leu	Ser	Ser	Glu	Arg	Leu	Ala	Ala	Phe	Gly	Ser	Arg	
			1055					1060					1065			
AAA	ATT	ATA	TTA	CGC	TTA	CAA	GTT	CCG	AAA	GGA	AGT	ACG	GGG	GCG	TAT	1248
Lys	Ile	Ile	Leu	Arg	Leu	Gln	Val	Pro	Lys	Gly	Ser	Thr	Gly	Ala	Tyr	
		1070					1075					1080				
TTA	AGT	GCC	ATT	GGT	GGA	TTT	GCA	AGT	GAA	AAA	GAG	ATC	CTA	CTT	GAT	1296
Leu	Ser	Ala	Ile	Gly	Gly	Phe	Ala	Ser	Glu	Lys	Glu	Ile	Leu	Leu	Asp	
	1085					1090					1095					
AAA	GAT	AGT	AAA	TAT	CAT	ATT	GAT	AAA	GCA	ACA	GAG	GTA	ATC	ATT	AAA	1344
Lys	Asp	Ser	Lys	Tyr	His	Ile	Asp	Lys	Ala	Thr	Glu	Val	Ile	Ile	Lys	
1100				1105						1110				1115		
GGT	GTT	AAG	CGA	TAT	GTA	GTG	GAT	GCA	ACA	TTA	TTA	ACA	AAT			1386
Gly	Val	Lys	Arg	Tyr	Val	Val	Asp	Ala	Thr	Leu	Leu	Thr	Asn			
				1120					1125							
TAAGGAG	ATG	AAA	AAT	ATG	AAG	AAA	AAG	TTA	GCA	AGT	GTT	GTA	ACC	TGT		1435
	Met	Lys	Asn	Met	Lys	Lys	Lys	Leu	Ala	Ser	Val	Val	Thr	Cys		
	1				5					10						
ATG	TTA	TTA	GCT	CCT	ATG	TTT	TTG	AAT	GGA	AAT	GTG	AAT	GCT	GTT	AAC	1483
Met	Leu	Leu	Ala	Pro	Met	Phe	Leu	Asn	Gly	Asn	Val	Asn	Ala	Val	Asn	
15					20					25					30	

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GCG GAT AGT AAA ATA AAT CAG ATT TCT ACA ACG CAG GAA AAC CAA CAG Ala Asp Ser Lys Ile Asn Gln Ile Ser Thr Thr Gln Glu Asn Gln Gln 35 40 45	1531
AAA GAG ATG GAC CGA AAG GGA TTA TTG GGA TAT TAT TTC AAA GGA AAA Lys Glu Met Asp Arg Lys Gly Leu Leu Gly Tyr Tyr Phe Lys Gly Lys 50 55 60	1579
GAT TTT AAT AAT CTT ACT ATG TTT GCA CCG ACA CGT GAT AAT ACC CTT Asp Phe Asn Asn Leu Thr Met Phe Ala Pro Thr Arg Asp Asn Thr Leu 65 70 75	1627
ATG TAT GAC CAA CAA ACA GCG AAT GCA TTA TTA GAT AAA AAA CAA CAA Met Tyr Asp Gln Gln Thr Ala Asn Ala Leu Leu Asp Lys Lys Gln Gln 80 85 90	1675
GAA TAT CAG TCC ATT CGT TGG ATT GGT TTG ATT CAG CGT AAA GAA ACG Glu Tyr Gln Ser Ile Arg Trp Ile Gly Leu Ile Gln Arg Lys Glu Thr 95 100 105 110	1723
GGC GAT TTC ACA TTT AAC TTA TCA AAG GAT GAA CAG GCA ATT ATA GAA Gly Asp Phe Thr Phe Asn Leu Ser Lys Asp Glu Gln Ala Ile Ile Glu 115 120 125	1771
ATC GAT GGG AAA ATC ATT TCT AAT AAA GGG AAA GAA AAG CAA GTT GTC Ile Asp Gly Lys Ile Ile Ser Asn Lys Gly Lys Glu Lys Gln Val Val 130 135 140	1819
CAT TTA GAA AAA GAA AAA TTA GTT CCA ATC AAA ATA GAG TAT CAA TCA His Leu Glu Lys Glu Lys Leu Val Pro Ile Lys Ile Glu Tyr Gln Ser 145 150 155	1867
GAT ACG AAA TTT AAT ATT GAT AGT AAA ACA TTT AAA GAA CTT AAA TTA Asp Thr Lys Phe Asn Ile Asp Ser Lys Thr Phe Lys Glu Leu Lys Leu 160 165 170	1915
TTT AAA ATA GAT AGT CAA AAC CAA TCT CAA CAA GTT CAA CTG AGA AAC Phe Lys Ile Asp Ser Gln Asn Gln Ser Gln Val Gln Leu Arg Asn 175 180 185 190	1963
CCT GAA TTT AAC AAA AAA GAA TCA CAG GAA TTT TTA GCA AAA GCA TCA Pro Glu Phe Asn Lys Lys Glu Ser Gln Glu Phe Leu Ala Lys Ala Ser 195 200 205	2011
AAA ACA AAC CTT TTT AAG CAA AAA ATG AAA AGA GAT ATT GAT GAA GAT Lys Thr Asn Leu Phe Lys Gln Lys Met Lys Arg Asp Ile Asp Glu Asp 210 215 220	2059
ACG GAT ACA GAT GGA GAC TCC ATT CCT GAT CTT TGG GAA GAA AAT GGG Thr Asp Thr Asp Gly Asp Ser Ile Pro Asp Leu Trp Glu Glu Asn Gly 225 230 235	2107
TAC ACG ATT CAA AAT AAA GTT GCT GTC AAA TGG GAT GAT TCG CTA GCA Tyr Thr Ile Gln Asn Lys Val Ala Val Lys Trp Asp Asp Ser Leu Ala 240 245 250	2155

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AGT AAG GGA TAT ACA AAA TTT GTT TCG AAT CCA TTA GAC AGC CAC ACA Ser Lys Gly Tyr Thr Lys Phe Val Ser Asn Pro Leu Asp Ser His Thr 255 260 265 270	2203
GTT GGC GAT CCC TAT ACT GAT TAT GAA AAG GCC GCA AGG GAT TTA GAT Val Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ala Arg Asp Leu Asp 275 280 285	2251
TTA TCA AAT GCA AAG GAA ACG TTC AAC CCA TTG GTA GCT GCT TTT CCA Leu Ser Asn Ala Lys Glu Thr Phe Asn Pro Leu Val Ala Ala Phe Pro 290 295 300	2299
AGT GTG AAT GTT AGT ATG GAA AAG GTG ATA TTA TCA CCA AAT GAA AAT Ser Val Asn Val Ser Met Glu Lys Val Ile Leu Ser Pro Asn Glu Asn 305 310 315	2347
TTA TCC AAT AGT GTA GAG TCT CAT TCA TCC ACG AAT TGG TCT TAT ACG Leu Ser Asn Ser Val Glu Ser His Ser Ser Thr Asn Trp Ser Tyr Thr 320 325 330	2395
AAT ACA GAA GGA GCT TCC ATT GAA GCT GGT GGC GGT CCA TTA GGC CTT Asn Thr Glu Gly Ala Ser Ile Glu Ala Gly Gly Gly Pro Leu Gly Leu 335 340 345 350	2443
TCT TTT GGC GTG AGT GTT ACT TAT CAA CAC TCT GAA ACA GTT GCA CAA Ser Phe Gly Val Ser Val Thr Tyr Gln His Ser Glu Thr Val Ala Gln 355 360 365	2491
GAA TGG GGA ACA TCT ACA GGA AAT ACT TCA CAA TTC AAT ACG GCT TCA Glu Trp Gly Thr Ser Thr Gly Asn Thr Ser Gln Phe Asn Thr Ala Ser 370 375 380	2539
GCG GGA TAT TTA AAT GCA AAT GTT CGG TAT AAC AAT GTA GGG ACT GGT Ala Gly Tyr Leu Asn Ala Asn Val Arg Tyr Asn Asn Val Gly Thr Gly 385 390 395	2587
GCC ATC TAT GAT GTA AAA CCT ACA ACA AGT TTT GTA TTA AAT AAC AAT Ala Ile Tyr Asp Val Lys Pro Thr Thr Ser Phe Val Leu Asn Asn Asn 400 405 410	2635
ACC ATC GCA ACG ATT ACA GCA AAA TCA AAT TCA ACA GCT TTA CGT ATA Thr Ile Ala Thr Ile Thr Ala Lys Ser Asn Ser Thr Ala Leu Arg Ile 415 420 425 430	2683
TCT CCG GGG GAT AGT TAT CCA GAA ATA GGA GAA AAC GCT ATT GCG ATT Ser Pro Gly Asp Ser Tyr Pro Glu Ile Gly Glu Asn Ala Ile Ala Ile 435 440 445	2731
ACA TCT ATG GAT GAT TTT AAT TCT CAT CCA ATT ACA TTA AAT AAA CAA Thr Ser Met Asp Asp Phe Asn Ser His Pro Ile Thr Leu Asn Lys Gln 450 455 460	2779
CAG GTA AAT CAA TTG ATA AAT AAT AAG CCA ATT ATG CTA GAG ACA GAC Gln Val Asn Gln Leu Ile Asn Asn Lys Pro Ile Met Leu Glu Thr Asp	2827

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465	470	475	
CAA ACA GAT GGT GTT TAT AAA ATA AGA GAT ACA CAT GGA AAT ATT GTA			2875
Gln Thr Asp Gly Val Tyr Lys Ile Arg Asp Thr His Gly Asn Ile Val			
480	485	490	
ACT GGT GGA GAA TGG AAT GGT GTA ACA CAA CAA ATT AAA GCA AAA ACA			2923
Thr Gly Gly Glu Trp Asn Gly Val Thr Gln Gln Ile Lys Ala Lys Thr			
495	500	505	510
GCG TCT ATT ATT GTG GAT GAC GGG AAA CAG GTA GCA GAA AAA CGT GTG			2971
Ala Ser Ile Ile Val Asp Asp Gly Lys Gln Val Ala Glu Lys Arg Val			
515	520	525	
GCG GCA AAA GAT TAT GGT CAT CCA GAA GAT AAA ACA CCA CCT TTA ACT			3019
Ala Ala Lys Asp Tyr Gly His Pro Glu Asp Lys Thr Pro Pro Leu Thr			
530	535	540	
TTA AAA GAT ACC CTG AAG CTT TCA TAC CCA GAT GAA ATA AAA GAA ACT			3067
Leu Lys Asp Thr Leu Lys Leu Ser Tyr Pro Asp Glu Ile Lys Glu Thr			
545	550	555	
AAT GGA TTG TTG TAC TAT GAT GAC AAA CCA ATC TAT GAA TCG AGT GTC			3115
Asn Gly Leu Leu Tyr Tyr Asp Asp Lys Pro Ile Tyr Glu Ser Ser Val			
560	565	570	
ATG ACT TAT CTG GAT GAA AAT ACG GCA AAA GAA GTC AAA AAA CAA ATA			3163
Met Thr Tyr Leu Asp Glu Asn Thr Ala Lys Glu Val Lys Lys Gln Ile			
575	580	585	590
AAT GAT ACA ACC GGA AAA TTT AAG GAT GTA AAT CAC TTA TAT GAT GTA			3211
Asn Asp Thr Thr Gly Lys Phe Lys Asp Val Asn His Leu Tyr Asp Val			
595	600	605	
AAA CTG ACT CCA AAA ATG AAT TTT ACG ATT AAA ATG GCT TCC TTG TAT			3259
Lys Leu Thr Pro Lys Met Asn Phe Thr Ile Lys Met Ala Ser Leu Tyr			
610	615	620	
GAT GGG GCT GAA AAT AAT CAT AAC TCT TTA GGA ACC TGG TAT TTA ACA			3307
Asp Gly Ala Glu Asn Asn His Asn Ser Leu Gly Thr Trp Tyr Leu Thr			
625	630	635	
TAT AAT GTT GCT GGT GGA AAT ACT GGG AAG AGA CAA TAT CGT TCA GCT			3355
Tyr Asn Val Ala Gly Gly Asn Thr Gly Lys Arg Gln Tyr Arg Ser Ala			
640	645	650	
CAT TCT TGT GCA CAT GTA GCT CTA TCT TCA GAA GCG AAA AAG AAA CTA			3403
His Ser Cys Ala His Val Ala Leu Ser Ser Glu Ala Lys Lys Lys Leu			
655	660	665	670
AAT CAA AAT GCG AAT TAC TAT CTT AGC ATG TAT ATG AAG GCT GAT TCT			3451
Asn Gln Asn Ala Asn Tyr Tyr Leu Ser Met Tyr Met Lys Ala Asp Ser			
675	680	685	
ACT ACG GAA CCT ACA ATA GAA GTA GCT GGG GAA AAA TCT GCA ATA ACA			3499

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Thr Thr Glu Pro Thr Ile Glu Val Ala Gly Glu Lys Ser Ala Ile Thr	
690 695 700	
AGT AAA AAA GTA AAA TTA AAT AAT CAA AAT TAT CAA AGA GTT GAT ATT	3547
Ser Lys Lys Val Lys Leu Asn Asn Gln Asn Tyr Gln Arg Val Asp Ile	
705 710 715	
TTA GTG AAA AAT TCT GAA AGA AAT CCA ATG GAT AAA ATA TAT ATA AGA	3595
Leu Val Lys Asn Ser Glu Arg Asn Pro Met Asp Lys Ile Tyr Ile Arg	
720 725 730	
GGA AAT GGC ACG ACA AAT GTT TAT GGG GAT GAT GTT ACT ATC CCA GAG	3643
Gly Asn Gly Thr Thr Asn Val Tyr Gly Asp Asp Val Thr Ile Pro Glu	
735 740 745 750	
GTA TCA GCT ATA AAT CCG GCT AGT CTA TCA GAT GAA GAA ATT CAA GAA	3691
Val Ser Ala Ile Asn Pro Ala Ser Leu Ser Asp Glu Glu Ile Gln Glu	
755 760 765	
ATA TTT AAA GAC TCA ACT ATT GAA TAT GGA AAT CCT AGT TTC GTT GCT	3739
Ile Phe Lys Asp Ser Thr Ile Glu Tyr Gly Asn Pro Ser Phe Val Ala	
770 775 780	
GAT GCC GTA ACA TTT AAA AAT ATA AAA CCT TTA CAA AAT TAT GTA AAG	3787
Asp Ala Val Thr Phe Lys Asn Ile Lys Pro Leu Gln Asn Tyr Val Lys	
785 790 795	
GAA TAT GAA ATA TAT CAT AAA TCT CAT CGA TAT GAA AAG AAA ACG GTC	3835
Glu Tyr Glu Ile Tyr His Lys Ser His Arg Tyr Glu Lys Lys Thr Val	
800 805 810	
TTT GAT ATC ATG GGT GTT CAT TAT GAG TAT AGT ATA GCT AGG GAA CAA	3883
Phe Asp Ile Met Gly Val His Tyr Glu Tyr Ser Ile Ala Arg Glu Gln	
815 820 825 830	
AAG AAA GCC GCA TAATTTTAAA AATAAACTC GTTAGAGTTT ATTTAGCATG	3935
Lys Lys Ala Ala	
GTATTTTAA GAATAATCAA TATGTTGAAC CGTTTGTAGC TGTTTTGGAA GGAATTTC	3995
TTTTATTTGG TCTCTTAAGT TGATGGGCAT GGGATATGTT CAGCATCCAA GCGTTTNGGG	4055
GGTTANAAAA TCCAATTTT	4074

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

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Met Gln Arg Met Glu Gly Lys Leu Phe Val Val Ser Lys Thr Leu Gln
 1           5           10           15

Val Val Thr Arg Thr Val Leu Leu Ser Thr Val Tyr Ser Ile Thr Leu
          20           25           30

Leu Asn Asn Val Val Ile Lys Ala Asp Gln Leu Asn Ile Asn Ser Gln
          35           40           45

Ser Lys Tyr Thr Asn Leu Gln Asn Leu Lys Ile Pro Asp Asn Ala Glu
          50           55           60

Asp Phe Lys Glu Asp Lys Gly Lys Ala Lys Glu Trp Gly Lys Glu Lys
65           70           75           80

Gly Glu Glu Trp Arg Pro Pro Ala Thr Glu Lys Gly Glu Met Asn Asn
          85           90           95

Phe Leu Asp Asn Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr
          100          105          110

Phe Ser Met Ala Gly Ser Cys Glu Asp Glu Ile Lys Asp Leu Glu Glu
          115          120          125

Ile Asp Lys Ile Phe Asp Lys Ala Asn Leu Ser Ser Ser Ile Ile Thr
          130          135          140

Tyr Lys Asn Val Glu Pro Ala Thr Ile Gly Phe Asn Lys Ser Leu Thr
          145          150          155          160

Glu Gly Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln
          165          170          175

Phe Leu Gly Lys Asp Met Lys Phe Asp Ser Tyr Leu Asp Thr His Leu
          180          185          190

Thr Ala Gln Gln Val Ser Ser Lys Lys Arg Val Ile Leu Lys Val Thr
          195          200          205

Val Pro Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile
          210          215          220

Leu Asn Asn Asn Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Val Leu
          225          230          235          240

His Val Asp Lys Val Ser Lys Val Val Lys Lys Gly Met Glu Cys Leu
          245          250          255

Gln Val Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile
          260          265          270

Asn Ala Glu Ala His Ser Trp Gly Met Lys Ile Tyr Glu Asp Trp Ala
          275          280          285

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Lys Asn Leu Thr Ala Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg
 290 295 300
 Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser
 305 310 315 320
 Gly Asn Glu Lys Leu Asp Ala Gln Leu Lys Asn Ile Ser Asp Ala Leu
 325 330 335
 Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly
 340 345 350
 Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys
 355 360 365
 Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr
 370 375 380
 Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg
 385 390 395 400
 Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr
 405 410 415
 Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp
 420 425 430
 Lys Asp Ser Lys Tyr His Ile Asp Lys Ala Thr Glu Val Ile Ile Lys
 435 440 445
 Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn
 450 455 460

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 834 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Lys Asn Met Lys Lys Lys Leu Ala Ser Val Val Thr Cys Met Leu
 1 5 10 15
 Leu Ala Pro Met Phe Leu Asn Gly Asn Val Asn Ala Val Asn Ala Asp
 20 25 30
 Ser Lys Ile Asn Gln Ile Ser Thr Thr Gln Glu Asn Gln Gln Lys Glu
 35 40 45

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Met Asp Arg Lys Gly Leu Leu Gly Tyr Tyr Phe Lys Gly Lys Asp Phe
 50 55 60

Asn Asn Leu Thr Met Phe Ala Pro Thr Arg Asp Asn Thr Leu Met Tyr
 65 70 75 80

Asp Gln Gln Thr Ala Asn Ala Leu Leu Asp Lys Lys Gln Gln Glu Tyr
 85 90 95

Gln Ser Ile Arg Trp Ile Gly Leu Ile Gln Arg Lys Glu Thr Gly Asp
 100 105 110

Phe Thr Phe Asn Leu Ser Lys Asp Glu Gln Ala Ile Ile Glu Ile Asp
 115 120 125

Gly Lys Ile Ile Ser Asn Lys Gly Lys Glu Lys Gln Val Val His Leu
 130 135 140

Glu Lys Glu Lys Leu Val Pro Ile Lys Ile Glu Tyr Gln Ser Asp Thr
 145 150 155 160

Lys Phe Asn Ile Asp Ser Lys Thr Phe Lys Glu Leu Lys Leu Phe Lys
 165 170 175

Ile Asp Ser Gln Asn Gln Ser Gln Gln Val Gln Leu Arg Asn Pro Glu
 180 185 190

Phe Asn Lys Lys Glu Ser Gln Glu Phe Leu Ala Lys Ala Ser Lys Thr
 195 200 205

Asn Leu Phe Lys Gln Lys Met Lys Arg Asp Ile Asp Glu Asp Thr Asp
 210 215 220

Thr Asp Gly Asp Ser Ile Pro Asp Leu Trp Glu Glu Asn Gly Tyr Thr
 225 230 235 240

Ile Gln Asn Lys Val Ala Val Lys Trp Asp Asp Ser Leu Ala Ser Lys
 245 250 255

Gly Tyr Thr Lys Phe Val Ser Asn Pro Leu Asp Ser His Thr Val Gly
 260 265 270

Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ala Arg Asp Leu Asp Leu Ser
 275 280 285

Asn Ala Lys Glu Thr Phe Asn Pro Leu Val Ala Ala Phe Pro Ser Val
 290 295 300

Asn Val Ser Met Glu Lys Val Ile Leu Ser Pro Asn Glu Asn Leu Ser
 305 310 315 320

Asn Ser Val Glu Ser His Ser Ser Thr Asn Trp Ser Tyr Thr Asn Thr
 325 330 335

Glu Gly Ala Ser Ile Glu Ala Gly Gly Gly Pro Leu Gly Leu Ser Phe

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340	345	350
Gly Val Ser Val Thr Tyr Gln His Ser Glu Thr Val Ala Gln Glu Trp		
355	360	365
Gly Thr Ser Thr Gly Asn Thr Ser Gln Phe Asn Thr Ala Ser Ala Gly		
370	375	380
Tyr Leu Asn Ala Asn Val Arg Tyr Asn Asn Val Gly Thr Gly Ala Ile		
385	390	395
Tyr Asp Val Lys Pro Thr Thr Ser Phe Val Leu Asn Asn Asn Thr Ile		
405	410	415
Ala Thr Ile Thr Ala Lys Ser Asn Ser Thr Ala Leu Arg Ile Ser Pro		
420	425	430
Gly Asp Ser Tyr Pro Glu Ile Gly Glu Asn Ala Ile Ala Ile Thr Ser		
435	440	445
Met Asp Asp Phe Asn Ser His Pro Ile Thr Leu Asn Lys Gln Gln Val		
450	455	460
Asn Gln Leu Ile Asn Asn Lys Pro Ile Met Leu Glu Thr Asp Gln Thr		
465	470	475
Asp Gly Val Tyr Lys Ile Arg Asp Thr His Gly Asn Ile Val Thr Gly		
485	490	495
Gly Glu Trp Asn Gly Val Thr Gln Gln Ile Lys Ala Lys Thr Ala Ser		
500	505	510
Ile Ile Val Asp Asp Gly Lys Gln Val Ala Glu Lys Arg Val Ala Ala		
515	520	525
Lys Asp Tyr Gly His Pro Glu Asp Lys Thr Pro Pro Leu Thr Leu Lys		
530	535	540
Asp Thr Leu Lys Leu Ser Tyr Pro Asp Glu Ile Lys Glu Thr Asn Gly		
545	550	555
Leu Leu Tyr Tyr Asp Asp Lys Pro Ile Tyr Glu Ser Ser Val Met Thr		
565	570	575
Tyr Leu Asp Glu Asn Thr Ala Lys Glu Val Lys Lys Gln Ile Asn Asp		
580	585	590
Thr Thr Gly Lys Phe Lys Asp Val Asn His Leu Tyr Asp Val Lys Leu		
595	600	605
Thr Pro Lys Met Asn Phe Thr Ile Lys Met Ala Ser Leu Tyr Asp Gly		
610	615	620
Ala Glu Asn Asn His Asn Ser Leu Gly Thr Trp Tyr Leu Thr Tyr Asn		
625	630	635
		640

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Val Ala Gly Gly Asn Thr Gly Lys Arg Gln Tyr Arg Ser Ala His Ser
 645 650 655
 Cys Ala His Val Ala Leu Ser Ser Glu Ala Lys Lys Lys Leu Asn Gln
 660 665 670
 Asn Ala Asn Tyr Tyr Leu Ser Met Tyr Met Lys Ala Asp Ser Thr Thr
 675 680 685
 Glu Pro Thr Ile Glu Val Ala Gly Glu Lys Ser Ala Ile Thr Ser Lys
 690 695 700
 Lys Val Lys Leu Asn Asn Gln Asn Tyr Gln Arg Val Asp Ile Leu Val
 705 710 715 720
 Lys Asn Ser Glu Arg Asn Pro Met Asp Lys Ile Tyr Ile Arg Gly Asn
 725 730 735
 Gly Thr Thr Asn Val Tyr Gly Asp Asp Val Thr Ile Pro Glu Val Ser
 740 745 750
 Ala Ile Asn Pro Ala Ser Leu Ser Asp Glu Glu Ile Gln Glu Ile Phe
 755 760 765
 Lys Asp Ser Thr Ile Glu Tyr Gly Asn Pro Ser Phe Val Ala Asp Ala
 770 775 780
 Val Thr Phe Lys Asn Ile Lys Pro Leu Gln Asn Tyr Val Lys Glu Tyr
 785 790 795 800
 Glu Ile Tyr His Lys Ser His Arg Tyr Glu Lys Lys Thr Val Phe Asp
 805 810 815
 Ile Met Gly Val His Tyr Glu Tyr Ser Ile Ala Arg Glu Gln Lys Lys
 820 825 830
 Ala Ala

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4041 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..4038
- (D) OTHER INFORMATION: /product= "VIP1A(a)/VIP2A(a) fusion

product"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG	AAA	AGA	ATG	GAG	GGA	AAG	TTG	TTT	ATG	GTG	TCA	AAA	AAA	TTA	CAA	48
Met	Lys	Arg	Met	Glu	Gly	Lys	Leu	Phe	Met	Val	Ser	Lys	Lys	Leu	Gln	
835					840					845					850	
GTA	GTT	ACT	AAA	ACT	GTA	TTG	CTT	AGT	ACA	GTT	TTC	TCT	ATA	TCT	TTA	96
Val	Val	Thr	Lys	Thr	Val	Leu	Leu	Ser	Thr	Val	Phe	Ser	Ile	Ser	Leu	
				855					860					865		
TTA	AAT	AAT	GAA	GTG	ATA	AAA	GCT	GAA	CAA	TTA	AAT	ATA	AAT	TCT	CAA	144
Leu	Asn	Asn	Glu	Val	Ile	Lys	Ala	Glu	Gln	Leu	Asn	Ile	Asn	Ser	Gln	
			870					875					880			
AGT	AAA	TAT	ACT	AAC	TTG	CAA	AAT	CTA	AAA	ATC	ACT	GAC	AAG	GTA	GAG	192
Ser	Lys	Tyr	Thr	Asn	Leu	Gln	Asn	Leu	Lys	Ile	Thr	Asp	Lys	Val	Glu	
		885					890					895				
GAT	TTT	AAA	GAA	GAT	AAG	GAA	AAA	GCG	AAA	GAA	TGG	GGG	AAA	GAA	AAA	240
Asp	Phe	Lys	Glu	Asp	Lys	Glu	Lys	Ala	Lys	Glu	Trp	Gly	Lys	Glu	Lys	
	900					905					910					
GAA	AAA	GAG	TGG	AAA	CTA	ACT	GCT	ACT	GAA	AAA	GGA	AAA	ATG	AAT	AAT	288
Glu	Lys	Glu	Trp	Lys	Leu	Thr	Ala	Thr	Glu	Lys	Gly	Lys	Met	Asn	Asn	
915					920					925					930	
TTT	TTA	GAT	AAT	AAA	AAT	GAT	ATA	AAG	ACA	AAT	TAT	AAA	GAA	ATT	ACT	336
Phe	Leu	Asp	Asn	Lys	Asn	Asp	Ile	Lys	Thr	Asn	Tyr	Lys	Glu	Ile	Thr	
				935					940					945		
TTT	TCT	ATG	GCA	GGC	TCA	TTT	GAA	GAT	GAA	ATA	AAA	GAT	TTA	AAA	GAA	384
Phe	Ser	Met	Ala	Gly	Ser	Phe	Glu	Asp	Glu	Ile	Lys	Asp	Leu	Lys	Glu	
			950					955					960			
ATT	GAT	AAG	ATG	TTT	GAT	AAA	ACC	AAT	CTA	TCA	AAT	TCT	ATT	ATC	ACC	432
Ile	Asp	Lys	Met	Phe	Asp	Lys	Thr	Asn	Leu	Ser	Asn	Ser	Ile	Ile	Thr	
		965					970					975				
TAT	AAA	AAT	GTG	GAA	CCG	ACA	ACA	ATT	GGA	TTT	AAT	AAA	TCT	TTA	ACA	480
Tyr	Lys	Asn	Val	Glu	Pro	Thr	Thr	Ile	Gly	Phe	Asn	Lys	Ser	Leu	Thr	
	980					985					990					
GAA	GGT	AAT	ACG	ATT	AAT	TCT	GAT	GCA	ATG	GCA	CAG	TTT	AAA	GAA	CAA	528
Glu	Gly	Asn	Thr	Ile	Asn	Ser	Asp	Ala	Met	Ala	Gln	Phe	Lys	Glu	Gln	
995					1000					1005					1010	
TTT	TTA	GAT	AGG	GAT	ATT	AAG	TTT	GAT	AGT	TAT	CTA	GAT	ACG	CAT	TTA	576
Phe	Leu	Asp	Arg	Asp	Ile	Lys	Phe	Asp	Ser	Tyr	Leu	Asp	Thr	His	Leu	
				1015					1020					1025		
ACT	GCT	CAA	CAA	GTT	TCC	AGT	AAA	GAA	AGA	GTT	ATT	TTG	AAG	GTT	ACG	624
Thr	Ala	Gln	Gln	Val	Ser	Ser	Lys	Glu	Arg	Val	Ile	Leu	Lys	Val	Thr	

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1030	1035	1040	
GTT CCG AGT GGG AAA GGT TCT ACT ACT CCA ACA AAA GCA GGT GTC ATT Val Pro Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile 1045 1050 1055			672
TTA AAT AAT AGT GAA TAC AAA ATG CTC ATT GAT AAT GGG TAT ATG GTC Leu Asn Asn Ser Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Met Val 1060 1065 1070			720
CAT GTA GAT AAG GTA TCA AAA GTG GTG AAA AAA GGG GTG GAG TGC TTA His Val Asp Lys Val Ser Lys Val Val Lys Lys Gly Val Glu Cys Leu 1075 1080 1085 1090			768
CAA ATT GAA GGG ACT TTA AAA AAG AGT CTT GAC TTT AAA AAT GAT ATA Gln Ile Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile 1095 1100 1105			816
AAT GCT GAA GCG CAT AGC TGG GGT ATG AAG AAT TAT GAA GAG TGG GCT Asn Ala Glu Ala His Ser Trp Gly Met Lys Asn Tyr Glu Glu Trp Ala 1110 1115 1120			864
AAA GAT TTA ACC GAT TCG CAA AGG GAA GCT TTA GAT GGG TAT GCT AGG Lys Asp Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg 1125 1130 1135			912
CAA GAT TAT AAA GAA ATC AAT AAT TAT TTA AGA AAT CAA GGC GGA AGT Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser 1140 1145 1150			960
GGA AAT GAA AAA CTA GAT GCT CAA ATA AAA AAT ATT TCT GAT GCT TTA Gly Asn Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala Leu 1155 1160 1165 1170			1008
GGG AAG AAA CCA ATA CCG GAA AAT ATT ACT GTG TAT AGA TGG TGT GGC Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly 1175 1180 1185			1056
ATG CCG GAA TTT GGT TAT CAA ATT AGT GAT CCG TTA CCT TCT TTA AAA Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys 1190 1195 1200			1104
GAT TTT GAA GAA CAA TTT TTA AAT ACA ATC AAA GAA GAC AAA GGA TAT Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr 1205 1210 1215			1152
ATG AGT ACA AGC TTA TCG AGT GAA CGT CTT GCA GCT TTT GGA TCT AGA Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg 1220 1225 1230			1200
AAA ATT ATA TTA CGA TTA CAA GTT CCG AAA GGA AGT ACG GGT GCG TAT Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr 1235 1240 1245 1250			1248
TTA AGT GCC ATT GGT GGA TTT GCA AGT GAA AAA GAG ATC CTA CTT GAT			1296

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Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp	
1255 1260 1265	
AAA GAT AGT AAA TAT CAT ATT GAT AAA GTA ACA GAG GTA ATT ATT AAA	1344
Lys Asp Ser Lys Tyr His Ile Asp Lys Val Thr Glu Val Ile Ile Lys	
1270 1275 1280	
GGT GTT AAG CGA TAT GTA GTG GAT GCA ACA TTA TTA ACA AAT ATG AAA	1392
Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn Met Lys	
1285 1290 1295	
AAT ATG AAG AAA AAG TTA GCA AGT GTT GTA ACG TGT ACG TTA TTA GCT	1440
Asn Met Lys Lys Lys Leu Ala Ser Val Val Thr Cys Thr Leu Leu Ala	
1300 1305 1310	
CCT ATG TTT TTG AAT GGA AAT GTG AAT GCT GTT TAC GCA GAC AGC AAA	1488
Pro Met Phe Leu Asn Gly Asn Val Asn Ala Val Tyr Ala Asp Ser Lys	
1315 1320 1325 1330	
ACA AAT CAA ATT TCT ACA ACA CAG AAA AAT CAA CAG AAA GAG ATG GAC	1536
Thr Asn Gln Ile Ser Thr Thr Gln Lys Asn Gln Gln Lys Glu Met Asp	
1335 1340 1345	
CGA AAA GGA TTA CTT GGG TAT TAT TTC AAA GGA AAA GAT TTT AGT AAT	1584
Arg Lys Gly Leu Leu Gly Tyr Tyr Phe Lys Gly Lys Asp Phe Ser Asn	
1350 1355 1360	
CTT ACT ATG TTT GCA CCG ACA CGT GAT AGT ACT CTT ATT TAT GAT CAA	1632
Leu Thr Met Phe Ala Pro Thr Arg Asp Ser Thr Leu Ile Tyr Asp Gln	
1365 1370 1375	
CAA ACA GCA AAT AAA CTA TTA GAT AAA AAA CAA CAA GAA TAT CAG TCT	1680
Gln Thr Ala Asn Lys Leu Leu Asp Lys Lys Gln Gln Glu Tyr Gln Ser	
1380 1385 1390	
ATT CGT TGG ATT GGT TTG ATT CAG AGT AAA GAA ACG GGA GAT TTC ACA	1728
Ile Arg Trp Ile Gly Leu Ile Gln Ser Lys Glu Thr Gly Asp Phe Thr	
1395 1400 1405 1410	
TTT AAC TTA TCT GAG GAT GAA CAG GCA ATT ATA GAA ATC AAT GGG AAA	1776
Phe Asn Leu Ser Glu Asp Glu Gln Ala Ile Ile Glu Ile Asn Gly Lys	
1415 1420 1425	
ATT ATT TCT AAT AAA GGG AAA GAA AAG CAA GTT GTC CAT TTA GAA AAA	1824
Ile Ile Ser Asn Lys Gly Lys Glu Lys Gln Val Val His Leu Glu Lys	
1430 1435 1440	
GGA AAA TTA GTT CCA ATC AAA ATA GAG TAT CAA TCA GAT ACA AAA TTT	1872
Gly Lys Leu Val Pro Ile Lys Ile Glu Tyr Gln Ser Asp Thr Lys Phe	
1445 1450 1455	
AAT ATT GAC AGT AAA ACA TTT AAA GAA CTT AAA TTA TTT AAA ATA GAT	1920
Asn Ile Asp Ser Lys Thr Phe Lys Glu Leu Lys Leu Phe Lys Ile Asp	
1460 1465 1470	

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AGT CAA AAC CAA CCC CAG CAA GTC CAG CAA GAT GAA CTG AGA AAT CCT Ser Gln Asn Gln Pro Gln Gln Val Gln Gln Asp Glu Leu Arg Asn Pro 1475 1480 1485 1490	1968
GAA TTT AAC AAG AAA GAA TCA CAG GAA TTC TTA GCG AAA CCA TCG AAA Glu Phe Asn Lys Lys Glu Ser Gln Glu Phe Leu Ala Lys Pro Ser Lys 1495 1500 1505	2016
ATA AAT CTT TTC ACT CAA AAA ATG AAA AGG GAA ATT GAT GAA GAC ACG Ile Asn Leu Phe Thr Gln Lys Met Lys Arg Glu Ile Asp Glu Asp Thr 1510 1515 1520	2064
GAT ACG GAT GGG GAC TCT ATT CCT GAC CTT TGG GAA GAA AAT GGG TAT Asp Thr Asp Gly Asp Ser Ile Pro Asp Leu Trp Glu Glu Asn Gly Tyr 1525 1530 1535	2112
ACG ATT CAA AAT AGA ATC GCT GTA AAG TGG GAC GAT TCT CTA GCA AGT Thr Ile Gln Asn Arg Ile Ala Val Lys Trp Asp Asp Ser Leu Ala Ser 1540 1545 1550	2160
AAA GGG TAT ACG AAA TTT GTT TCA AAT CCA CTA GAA AGT CAC ACA GTT Lys Gly Tyr Thr Lys Phe Val Ser Asn Pro Leu Glu Ser His Thr Val 1555 1560 1565 1570	2208
GGT GAT CCT TAT ACA GAT TAT GAA AAG GCA GCA AGA GAT CTA GAT TTG Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ala Arg Asp Leu Asp Leu 1575 1580 1585	2256
TCA AAT GCA AAG GAA ACG TTT AAC CCA TTG GTA GCT GCT TTT CCA AGT Ser Asn Ala Lys Glu Thr Phe Asn Pro Leu Val Ala Ala Phe Pro Ser 1590 1595 1600	2304
GTG AAT GTT AGT ATG GAA AAG GTG ATA TTA TCA CCA AAT GAA AAT TTA Val Asn Val Ser Met Glu Lys Val Ile Leu Ser Pro Asn Glu Asn Leu 1605 1610 1615	2352
TCC AAT AGT GTA GAG TCT CAT TCA TCC ACG AAT TGG TCT TAT ACA AAT Ser Asn Ser Val Glu Ser His Ser Ser Thr Asn Trp Ser Tyr Thr Asn 1620 1625 1630	2400
ACA GAA GGT GCT TCT GTT GAA GCG GGG ATT GGA CCA AAA GGT ATT TCG Thr Glu Gly Ala Ser Val Glu Ala Gly Ile Gly Pro Lys Gly Ile Ser 1635 1640 1645 1650	2448
TTC GGA GTT AGC GTA AAC TAT CAA CAC TCT GAA ACA GTT GCA CAA GAA Phe Gly Val Ser Val Asn Tyr Gln His Ser Glu Thr Val Ala Gln Glu 1655 1660 1665	2496
TGG GGA ACA TCT ACA GGA AAT ACT TCG CAA TTC AAT ACG GCT TCA GCG Trp Gly Thr Ser Thr Gly Asn Thr Ser Gln Phe Asn Thr Ala Ser Ala 1670 1675 1680	2544
GGA TAT TTA AAT GCA AAT GTT CGA TAT AAC AAT GTA GGA ACT GGT GCC Gly Tyr Leu Asn Ala Asn Val Arg Tyr Asn Asn Val Gly Thr Gly Ala 1685 1690 1695	2592

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ATC TAC GAT GTA AAA CCT ACA ACA AGT TTT GTA TTA AAT AAC GAT ACT Ile Tyr Asp Val Lys Pro Thr Thr Ser Phe Val Leu Asn Asn Asp Thr 1700 1705 1710	2640
ATC GCA ACT ATT ACG GCG AAA TCT AAT TCT ACA GCC TTA AAT ATA TCT Ile Ala Thr Ile Thr Ala Lys Ser Asn Ser Thr Ala Leu Asn Ile Ser 1715 1720 1725 1730	2688
CCT GGA GAA AGT TAC CCG AAA AAA GGA CAA AAT GGA ATC GCA ATA ACA Pro Gly Glu Ser Tyr Pro Lys Lys Gly Gln Asn Gly Ile Ala Ile Thr 1735 1740 1745	2736
TCA ATG GAT GAT TTT AAT TCC CAT CCG ATT ACA TTA AAT AAA AAA CAA Ser Met Asp Asp Phe Asn Ser His Pro Ile Thr Leu Asn Lys Lys Gln 1750 1755 1760	2784
GTA GAT AAT CTG CTA AAT AAT AAA CCT ATG ATG TTG GAA ACA AAC CAA Val Asp Asn Leu Leu Asn Asn Lys Pro Met Met Leu Glu Thr Asn Gln 1765 1770 1775	2832
ACA GAT GGT GTT TAT AAG ATA AAA GAT ACA CAT GGA AAT ATA GTA ACT Thr Asp Gly Val Tyr Lys Ile Lys Asp Thr His Gly Asn Ile Val Thr 1780 1785 1790	2880
GGC GGA GAA TGG AAT GGT GTC ATA CAA CAA ATC AAG GCT AAA ACA GCG Gly Gly Glu Trp Asn Gly Val Ile Gln Gln Ile Lys Ala Lys Thr Ala 1795 1800 1805 1810	2928
TCT ATT ATT GTG GAT GAT GGG GAA CGT GTA GCA GAA AAA CGT GTA GCG Ser Ile Ile Val Asp Asp Gly Glu Arg Val Ala Glu Lys Arg Val Ala 1815 1820 1825	2976
GCA AAA GAT TAT GAA AAT CCA GAA GAT AAA ACA CCG TCT TTA ACT TTA Ala Lys Asp Tyr Glu Asn Pro Glu Asp Lys Thr Pro Ser Leu Thr Leu 1830 1835 1840	3024
AAA GAT GCC CTG AAG CTT TCA TAT CCA GAT GAA ATA AAA GAA ATA GAG Lys Asp Ala Leu Lys Leu Ser Tyr Pro Asp Glu Ile Lys Glu Ile Glu 1845 1850 1855	3072
GGA TTA TTA TAT TAT AAA AAC AAA CCG ATA TAC GAA TCG AGC GTT ATG Gly Leu Leu Tyr Tyr Lys Asn Lys Pro Ile Tyr Glu Ser Ser Val Met 1860 1865 1870	3120
ACT TAC TTA GAT GAA AAT ACA GCA AAA GAA GTG ACC AAA CAA TTA AAT Thr Tyr Leu Asp Glu Asn Thr Ala Lys Glu Val Thr Lys Gln Leu Asn 1875 1880 1885 1890	3168
GAT ACC ACT GGG AAA TTT AAA GAT GTA AGT CAT TTA TAT GAT GTA AAA Asp Thr Thr Gly Lys Phe Lys Asp Val Ser His Leu Tyr Asp Val Lys 1895 1900 1905	3216
CTG ACT CCA AAA ATG AAT GTT ACA ATC AAA TTG TCT ATA CTT TAT GAT Leu Thr Pro Lys Met Asn Val Thr Ile Lys Leu Ser Ile Leu Tyr Asp	3264

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1910	1915	1920	
AAT GCT GAG TCT AAT GAT AAC TCA ATT GGT AAA TGG ACA AAC ACA AAT Asn Ala Glu Ser Asn Asp Asn Ser Ile Gly Lys Trp Thr Asn Thr Asn 1925 1930 1935			3312
ATT GTT TCA GGT GGA AAT AAC GGA AAA AAA CAA TAT TCT TCT AAT AAT Ile Val Ser Gly Gly Asn Asn Gly Lys Lys Gln Tyr Ser Ser Asn Asn 1940 1945 1950			3360
CCG GAT GCT AAT TTG ACA TTA AAT ACA GAT GCT CAA GAA AAA TTA AAT Pro Asp Ala Asn Leu Thr Leu Asn Thr Asp Ala Gln Glu Lys Leu Asn 1955 1960 1965 1970			3408
AAA AAT CGT GAC TAT TAT ATA AGT TTA TAT ATG AAG TCA GAA AAA AAC Lys Asn Arg Asp Tyr Tyr Ile Ser Leu Tyr Met Lys Ser Glu Lys Asn 1975 1980 1985			3456
ACA CAA TGT GAG ATT ACT ATA GAT GGG GAG ATT TAT CCG ATC ACT ACA Thr Gln Cys Glu Ile Thr Ile Asp Gly Glu Ile Tyr Pro Ile Thr Thr 1990 1995 2000			3504
AAA ACA GTG AAT GTG AAT AAA GAC AAT TAC AAA AGA TTA GAT ATT ATA Lys Thr Val Asn Val Asn Lys Asp Asn Tyr Lys Arg Leu Asp Ile Ile 2005 2010 2015			3552
GCT CAT AAT ATA AAA AGT AAT CCA ATT TCT TCA CTT CAT ATT AAA ACG Ala His Asn Ile Lys Ser Asn Pro Ile Ser Ser Leu His Ile Lys Thr 2020 2025 2030			3600
AAT GAT GAA ATA ACT TTA TTT TGG GAT GAT ATT TCT ATA ACA GAT GTA Asn Asp Glu Ile Thr Leu Phe Trp Asp Asp Ile Ser Ile Thr Asp Val 2035 2040 2045 2050			3648
GCA TCA ATA AAA CCG GAA AAT TTA ACA GAT TCA GAA ATT AAA CAG ATT Ala Ser Ile Lys Pro Glu Asn Leu Thr Asp Ser Glu Ile Lys Gln Ile 2055 2060 2065			3696
TAT AGT AGG TAT GGT ATT AAG TTA GAA GAT GGA ATC CTT ATT GAT AAA Tyr Ser Arg Tyr Gly Ile Lys Leu Glu Asp Gly Ile Leu Ile Asp Lys 2070 2075 2080			3744
AAA GGT GGG ATT CAT TAT GGT GAA TTT ATT AAT GAA GCT AGT TTT AAT Lys Gly Gly Ile His Tyr Gly Glu Phe Ile Asn Glu Ala Ser Phe Asn 2085 2090 2095			3792
ATT GAA CCA TTG CAA AAT TAT GTG ACC AAA TAT GAA GTT ACT TAT AGT Ile Glu Pro Leu Gln Asn Tyr Val Thr Lys Tyr Glu Val Thr Tyr Ser 2100 2105 2110			3840
AGT GAG TTA GGA CCA AAC GTG AGT GAC ACA CTT GAA AGT GAT AAA ATT Ser Glu Leu Gly Pro Asn Val Ser Asp Thr Leu Glu Ser Asp Lys Ile 2115 2120 2125 2130			3888
TAC AAG GAT GGG ACA ATT AAA TTT GAT TTT ACC AAA TAT AGT AAA AAT			3936

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Tyr Lys Asp Gly Thr Ile Lys Phe Asp Phe Thr Lys Tyr Ser Lys Asn	
2135 2140 2145	
GAA CAA GGA TTA TTT TAT GAC AGT GGA TTA AAT TGG GAC TTT AAA ATT	3984
Glu Gln Gly Leu Phe Tyr Asp Ser Gly Leu Asn Trp Asp Phe Lys Ile	
2150 2155 2160	
AAT GCT ATT ACT TAT GAT GGT AAA GAG ATG AAT GTT TTT CAT AGA TAT	4032
Asn Ala Ile Thr Tyr Asp Gly Lys Glu Met Asn Val Phe His Arg Tyr	
2165 2170 2175	
AAT AAA TAG	4041
Asn Lys	
2180	

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1346 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Lys Arg Met Glu Gly Lys Leu Phe Met Val Ser Lys Lys Leu Gln	
1 5 10 15	
Val Val Thr Lys Thr Val Leu Leu Ser Thr Val Phe Ser Ile Ser Leu	
20 25 30	
Leu Asn Asn Glu Val Ile Lys Ala Glu Gln Leu Asn Ile Asn Ser Gln	
35 40 45	
Ser Lys Tyr Thr Asn Leu Gln Asn Leu Lys Ile Thr Asp Lys Val Glu	
50 55 60	
Asp Phe Lys Glu Asp Lys Glu Lys Ala Lys Glu Trp Gly Lys Glu Lys	
65 70 75 80	
Glu Lys Glu Trp Lys Leu Thr Ala Thr Glu Lys Gly Lys Met Asn Asn	
85 90 95	
Phe Leu Asp Asn Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr	
100 105 110	
Phe Ser Met Ala Gly Ser Phe Glu Asp Glu Ile Lys Asp Leu Lys Glu	
115 120 125	
Ile Asp Lys Met Phe Asp Lys Thr Asn Leu Ser Asn Ser Ile Ile Thr	
130 135 140	
Tyr Lys Asn Val Glu Pro Thr Thr Ile Gly Phe Asn Lys Ser Leu Thr	

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145 150 155 160
 Glu Gly Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln
 165 170 175
 Phe Leu Asp Arg Asp Ile Lys Phe Asp Ser Tyr Leu Asp Thr His Leu
 180 185 190
 Thr Ala Gln Gln Val Ser Ser Lys Glu Arg Val Ile Leu Lys Val Thr
 195 200 205
 Val Pro Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile
 210 215 220
 Leu Asn Asn Ser Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Met Val
 225 230 235 240
 His Val Asp Lys Val Ser Lys Val Val Lys Lys Gly Val Glu Cys Leu
 245 250 255
 Gln Ile Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile
 260 265 270
 Asn Ala Glu Ala His Ser Trp Gly Met Lys Asn Tyr Glu Glu Trp Ala
 275 280 285
 Lys Asp Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg
 290 295 300
 Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser
 305 310 315 320
 Gly Asn Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala Leu
 325 330 335
 Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly
 340 345 350
 Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys
 355 360 365
 Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr
 370 375 380
 Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg
 385 390 395 400
 Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr
 405 410 415
 Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp
 420 425 430
 Lys Asp Ser Lys Tyr His Ile Asp Lys Val Thr Glu Val Ile Ile Lys
 435 440 445

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Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn Met Lys
 450 455 460

Asn Met Lys Lys Lys Leu Ala Ser Val Val Thr Cys Thr Leu Leu Ala
 465 470 475 480

Pro Met Phe Leu Asn Gly Asn Val Asn Ala Val Tyr Ala Asp Ser Lys
 485 490 495

Thr Asn Gln Ile Ser Thr Thr Gln Lys Asn Gln Gln Lys Glu Met Asp
 500 505 510

Arg Lys Gly Leu Leu Gly Tyr Tyr Phe Lys Gly Lys Asp Phe Ser Asn
 515 520 525

Leu Thr Met Phe Ala Pro Thr Arg Asp Ser Thr Leu Ile Tyr Asp Gln
 530 535 540

Gln Thr Ala Asn Lys Leu Leu Asp Lys Lys Gln Gln Glu Tyr Gln Ser
 545 550 555 560

Ile Arg Trp Ile Gly Leu Ile Gln Ser Lys Glu Thr Gly Asp Phe Thr
 565 570 575

Phe Asn Leu Ser Glu Asp Glu Gln Ala Ile Ile Glu Ile Asn Gly Lys
 580 585 590

Ile Ile Ser Asn Lys Gly Lys Glu Lys Gln Val Val His Leu Glu Lys
 595 600 605

Gly Lys Leu Val Pro Ile Lys Ile Glu Tyr Gln Ser Asp Thr Lys Phe
 610 615 620

Asn Ile Asp Ser Lys Thr Phe Lys Glu Leu Lys Leu Phe Lys Ile Asp
 625 630 635 640

Ser Gln Asn Gln Pro Gln Gln Val Gln Gln Asp Glu Leu Arg Asn Pro
 645 650 655

Glu Phe Asn Lys Lys Glu Ser Gln Glu Phe Leu Ala Lys Pro Ser Lys
 660 665 670

Ile Asn Leu Phe Thr Gln Lys Met Lys Arg Glu Ile Asp Glu Asp Thr
 675 680 685

Asp Thr Asp Gly Asp Ser Ile Pro Asp Leu Trp Glu Glu Asn Gly Tyr
 690 695 700

Thr Ile Gln Asn Arg Ile Ala Val Lys Trp Asp Asp Ser Leu Ala Ser
 705 710 715 720

Lys Gly Tyr Thr Lys Phe Val Ser Asn Pro Leu Glu Ser His Thr Val
 725 730 735

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Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ala Arg Asp Leu Asp Leu
 740 745 750
 Ser Asn Ala Lys Glu Thr Phe Asn Pro Leu Val Ala Ala Phe Pro Ser
 755 760 765
 Val Asn Val Ser Met Glu Lys Val Ile Leu Ser Pro Asn Glu Asn Leu
 770 775 780
 Ser Asn Ser Val Glu Ser His Ser Ser Thr Asn Trp Ser Tyr Thr Asn
 785 790 795 800
 Thr Glu Gly Ala Ser Val Glu Ala Gly Ile Gly Pro Lys Gly Ile Ser
 805 810 815
 Phe Gly Val Ser Val Asn Tyr Gln His Ser Glu Thr Val Ala Gln Glu
 820 825 830
 Trp Gly Thr Ser Thr Gly Asn Thr Ser Gln Phe Asn Thr Ala Ser Ala
 835 840 845
 Gly Tyr Leu Asn Ala Asn Val Arg Tyr Asn Asn Val Gly Thr Gly Ala
 850 855 860
 Ile Tyr Asp Val Lys Pro Thr Thr Ser Phe Val Leu Asn Asn Asp Thr
 865 870 875 880
 Ile Ala Thr Ile Thr Ala Lys Ser Asn Ser Thr Ala Leu Asn Ile Ser
 885 890 895
 Pro Gly Glu Ser Tyr Pro Lys Lys Gly Gln Asn Gly Ile Ala Ile Thr
 900 905 910
 Ser Met Asp Asp Phe Asn Ser His Pro Ile Thr Leu Asn Lys Lys Gln
 915 920 925
 Val Asp Asn Leu Leu Asn Asn Lys Pro Met Met Leu Glu Thr Asn Gln
 930 935 940
 Thr Asp Gly Val Tyr Lys Ile Lys Asp Thr His Gly Asn Ile Val Thr
 945 950 955 960
 Gly Gly Glu Trp Asn Gly Val Ile Gln Gln Ile Lys Ala Lys Thr Ala
 965 970 975
 Ser Ile Ile Val Asp Asp Gly Glu Arg Val Ala Glu Lys Arg Val Ala
 980 985 990
 Ala Lys Asp Tyr Glu Asn Pro Glu Asp Lys Thr Pro Ser Leu Thr Leu
 995 1000 1005
 Lys Asp Ala Leu Lys Leu Ser Tyr Pro Asp Glu Ile Lys Glu Ile Glu
 1010 1015 1020
 Gly Leu Leu Tyr Tyr Lys Asn Lys Pro Ile Tyr Glu Ser Ser Val Met

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1025	1030	1035	1040
Thr Tyr Leu Asp Glu Asn Thr Ala Lys Glu Val Thr Lys Gln Leu Asn			
1045		1050	1055
Asp Thr Thr Gly Lys Phe Lys Asp Val Ser His Leu Tyr Asp Val Lys			
1060	1065		1070
Leu Thr Pro Lys Met Asn Val Thr Ile Lys Leu Ser Ile Leu Tyr Asp			
1075	1080		1085
Asn Ala Glu Ser Asn Asp Asn Ser Ile Gly Lys Trp Thr Asn Thr Asn			
1090	1095	1100	
Ile Val Ser Gly Gly Asn Asn Gly Lys Lys Gln Tyr Ser Ser Asn Asn			
1105	1110	1115	1120
Pro Asp Ala Asn Leu Thr Leu Asn Thr Asp Ala Gln Glu Lys Leu Asn			
1125	1130		1135
Lys Asn Arg Asp Tyr Tyr Ile Ser Leu Tyr Met Lys Ser Glu Lys Asn			
1140	1145		1150
Thr Gln Cys Glu Ile Thr Ile Asp Gly Glu Ile Tyr Pro Ile Thr Thr			
1155	1160		1165
Lys Thr Val Asn Val Asn Lys Asp Asn Tyr Lys Arg Leu Asp Ile Ile			
1170	1175	1180	
Ala His Asn Ile Lys Ser Asn Pro Ile Ser Ser Leu His Ile Lys Thr			
1185	1190	1195	1200
Asn Asp Glu Ile Thr Leu Phe Trp Asp Asp Ile Ser Ile Thr Asp Val			
1205	1210		1215
Ala Ser Ile Lys Pro Glu Asn Leu Thr Asp Ser Glu Ile Lys Gln Ile			
1220	1225		1230
Tyr Ser Arg Tyr Gly Ile Lys Leu Glu Asp Gly Ile Leu Ile Asp Lys			
1235	1240		1245
Lys Gly Gly Ile His Tyr Gly Glu Phe Ile Asn Glu Ala Ser Phe Asn			
1250	1255	1260	
Ile Glu Pro Leu Gln Asn Tyr Val Thr Lys Tyr Glu Val Thr Tyr Ser			
1265	1270	1275	1280
Ser Glu Leu Gly Pro Asn Val Ser Asp Thr Leu Glu Ser Asp Lys Ile			
1285	1290		1295
Tyr Lys Asp Gly Thr Ile Lys Phe Asp Phe Thr Lys Tyr Ser Lys Asn			
1300	1305		1310
Glu Gln Gly Leu Phe Tyr Asp Ser Gly Leu Asn Trp Asp Phe Lys Ile			
1315	1320		1325

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Asn Ala Ile Thr Tyr Asp Gly Lys Glu Met Asn Val Phe His Arg Tyr
 1330 1335 1340

Asn Lys
 1345

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..1386
- (D) OTHER INFORMATION: /note= "Maize optimized DNA sequence for VIP2A(a) protein from AB78"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATGAAGCGCA TGGAGGGCAA GCTGTTTCATG GTGAGCAAGA AGCTCCAGGT GGTGACCAAG	60
ACCGTGCTGC TGAGCACCGT GTTCAGCATC AGCCTGCTGA ACAACGAGGT GATCAAGGCC	120
GAGCAGCTGA ACATCAACAG CCAGAGCAAG TACACCAACC TCCAGAACCT GAAGATCACC	180
GACAAGGTGG AGGACTTCAA GGAGGACAAG GAGAAGGCCA AGGAGTGGGG CAAGGAGAAG	240
GAGAAGGAGT GGAAGCTTAC CGCCACCGAG AAGGGCAAGA TGAACAACTT CCTGGACAAC	300
AAGAACGACA TCAAGACCAA CTACAAGGAG ATCACCTTCA GCATGGCCGG CAGCTTOGAG	360
GACGAGATCA AGGACCTGAA GGAGATCGAC AAGATGTTTG ACAAGACCAA CCTGAGCAAC	420
AGCATCATCA CCTACAAGAA CGTGGAGCCC ACCACCATCG GCTTCAACAA GAGCCTGACC	480
GAGGGCAACA CCATCAACAG CGACGCCATG GCCCAGTTCA AGGAGCAGTT CCTGGACCGC	540
GACATCAAGT TCGACAGCTA CCTGGACACC CACCTGACCG CCCAGCAGGT GAGCAGCAAG	600
GAGCGCGTGA TCCTGAAGGT GACCGTCCCC AGCGGCAAGG GCAGCACCAC CCCACCAAG	660
GCCGGCGTGA TCCTGAACAA CAGCGAGTAC AAGATGCTGA TCGACAACGG CTACATGGTG	720
CACGTGGACA AGGTGAGCAA GGTGGTGAAG AAGGGCGTGG AGTGCCTCCA GATCGAGGGC	780
ACCCTGAAGA AGAGTCTAGA CTTCAAGAAC GACATCAACG CCGAGGCCCA CAGCTGGGGC	840

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ATGAAGAACT ACGAGGAGTG GGCCAAGGAC CTGACCGACA GCCAGCGCGA GGCCCTGGAC      900
GGCTACGCCC GCCAGGACTA CAAGGAGATC AACAACTACC TGCGCAACCA GGGCGGCAGC      960
GGCAACGAGA AGCTGGACGC CCAGATCAAG AACATCAGCG ACGCCCTGGG CAAGAAGCCC      1020
ATCCCCGAGA ACATCACCGT GTACCGCTGG TGCGGCATGC CCGAGTTCGG CTACCAGATC      1080
AGCGACCCCC TGCCCAGCCT GAAGGACTTC GAGGAGCAGT TCCTGAACAC CATCAAGGAG      1140
GACAAGGGCT ACATGAGCAC CAGCCTGAGC AGCGAGCGCC TGGCCGCCTT CGGCAGCCGC      1200
AAGATCATCC TGCGCCTGCA GGTGCCCAAG GGCAGCACCG GCGCTACCT GAGCGCCATC      1260
GGCGGCTTCG CCAGCGAGAA GGAGATCCTG CTGGACAAGG ACAGCAAGTA CCACATCGAC      1320
AAGGTGACCG AGGTGATCAT CAAGGGCGTG AAGCGCTACG TGGTGGACGC CACCCTGCTG      1380
ACCAACTAGA TCTGAGCTC                                     1399

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(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "Secretion signal peptide to secrete VIP2 out of a cell"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly Val
1           5           10           15
His Cys Leu

```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

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(A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1..2655

(D) OTHER INFORMATION: /note= "maize optimized DNA
sequence encoding VIPLA(a)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGAAGAACA TGAAGAAGAA GCTGGCCAGC GTGGTGACCT GCACCCTGCT GGCCCCCATG	60
TTCCTGAACG GCAACGTGAA CGCCGTGTAC GCCGACAGCA AGACCAACCA GATCAGCACC	120
ACCCAGAAGA ACCAGCAGAA GGAGATGGAC CGCAAGGGCC TGCTGGGCTA CTACTTCAAG	180
GGCAAGGACT TCAGCAACCT GACCATGTTC GCCCCACGC GTGACAGCAC CCTGATCTAC	240
GACCAGCAGA CCGCCAACAA GCTGCTGGAC AAGAAGCAGC AGGAGTACCA GAGCATCCGC	300
TGGATCGGCC TGATCCAGAG CAAGGAGACC GGCGACTTCA CTTCAACCT GAGCGAGGAC	360
GAGCAGGCCA TCATCGAGAT CAACGGCAAG ATCATCAGCA ACAAGGGCAA GGAGAAGCAG	420
GTGGTGACCC TGGAGAAGGG CAAGCTGGTG CCCATCAAGA TCGAGTACCA GAGCGACACC	480
AAGTTCAACA TCGACAGCAA GACCTTCAAG GAGCTGAAGC TTTTCAAGAT CGACAGCCAG	540
AACCAGCCCC AGCAGGTGCA GCAGGACGAG CTGCGCAACC CCGAGTTCAA CAAGAAGGAG	600
AGCCAGGAGT TCCTGGCCAA GCCCAGCAAG ATCAACCTGT TCACCCAGCA GATGAAGCGC	660
GAGATCGACG AGGACACCGA CACCGACGGC GACAGCATCC CCGACCTGTG GGAGGAGAAC	720
GGCTACACCA TCCAGAACCG CATCGCOGTG AAGTGGGACG ACAGCCTGGC TAGCAAGGGC	780
TACACCAAGT TCGTGAGCAA CCCCCTGGAG AGCCACACCG TGGGCGACCC CTACACCGAC	840
TACGAGAAGG CCGCCCGCGA CCTGGACCTG AGCAACGCCA AGGAGACCTT CAACCCCCTG	900
GTGGCCGCCT TCCCCAGCGT GAACGTGAGC ATGGAGAAGG TGATCCTGAG CCCCACGAG	960
AACCTGAGCA ACAGCGTGGA GAGCCACTCG AGCACCAACT GGAGCTACAC CAACACCGAG	1020
GGCGCCAGCG TGGAGGCCGG CATCGGTCCC AAGGGCATCA GCTTCGGCGT GAGCGTGAAC	1080
TACCAGCACA GCGAGACCGT GGCCCAGGAG TGGGGCACCA GCACCGGCAA CACCAGCCAG	1140
TTCAACACCG CCAGCGCCGG CTACCTGAAC GCCAACGTGC GCTACAACAA CGTGGGCACC	1200
GGCGCCATCT ACGACGTGAA GCCCACCACC AGCTTCGTGC TGAACAACGA CACCATCGCC	1260

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ACCATCACCG CCAAGTCGAA TTCCACCGCC CTGAACATCA GCCCCGGCGA GAGCTACCCC	1320
AAGAAGGGCC AGAACGGCAT CGCCATCACC AGCATGGACG ACTTCAACAG CCACCCCATC	1380
ACCCTGAACA AGAAGCAGGT GGACAACCTG CTGAACAACA AGCCCATGAT GCTGGAGACC	1440
AACCAGACCG ACGGCGTCTA CAAGATCAAG GACACCCACG GCAACATCGT GACGGGCGGC	1500
GAGTGGAACG GCGTGATCCA GCAGATCAAG GCCAAGACCG CCAGCATCAT CGTCGACGAC	1560
GGCGAGCGCG TGGCCGAGAA GCGOGTGGCC GCCAAGGACT ACGAGAACCC CGAGGACAAG	1620
ACCCCCAGCC TGACCCTGAA GGACGCCCTG AAGCTGAGCT ACCCGACGA GATCAAGGAG	1680
ATCGAGGGCT TGCTGTACTA CAAGAACAAG CCCATCTACG AGAGCAGCGT GATGACCTAT	1740
CTAGACGAGA ACACCGCCAA GGAGGTGACC AAGCAGCTGA ACGACACCAC CGGCAAGTTC	1800
AAGGACGTGA GCCACCTGTA CGACGTGAAG CTGACCCCCA AGATGAACGT GACCATCAAG	1860
CTGAGCATCC TGTACGACAA CGCOGAGAGC AACGACAACA GCATCGGCAA GTGGACCAAC	1920
ACCAACATCG TGAGCGGCGG CAACAACGGC AAGAAGCAGT ACAGCAGCAA CAACCCCGAC	1980
GCCAACCTGA CCCTGAACAC CGACGCCCAG GAGAAGCTGA ACAAGAACCG CGACTACTAC	2040
ATCAGCCTGT ACATGAAGAG CGAGAAGAAC ACCCAGTGCG AGATCACCAT CGACGGCGAG	2100
ATATACCCCA TCACCACCAA GACCGTGAAC GTGAACAAGG ACAACTACAA GCGCCTGGAC	2160
ATCATCGCCC ACAACATCAA GAGCAACCCC ATCAGCAGCC TGCACATCAA GACCAACGAC	2220
GAGATCACCC TGTTCCTGGGA CGACATATCG ATTACCGACG TCGCCAGCAT CAAGCCCGAG	2280
AACCTGACCG ACAGCGAGAT CAAGCAGATA TACAGTCGCT ACGGCATCAA GCTGGAGGAC	2340
GGCATCCTGA TCGACAAGAA AGGCGGCATC CACTACGGCG AGTTCATCAA CGAGGCCAGC	2400
TTCAACATCG AGCCCCTGCA GAACTACGTG ACCAAGTACG AGGTGACCTA CAGCAGCGAG	2460
CTGGGCCCCA ACGTGAGCGA CACCTGGAG AGCGACAAGA TTTACAAGGA CGGCACCATC	2520
AAGTTCGACT TCACCAAGTA CAGCAAGAAC GAGCAGGGCC TGTTCTACGA CAGCGGCCTG	2580
AACTGGGACT TCAAGATCAA CGCCATCACC TACGACGGCA AGGAGATGAA CGTGTTCCAC	2640
CGCTACAACA AGTAG	2655

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1..1389

(D) OTHER INFORMATION: /note= "maize optimized DNA
sequence encoding VIP2A(a)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGAAGCGCA TGGAGGGCAA GCTGTTTCATG GTGAGCAAGA AGCTCCAGGT GGTGACCAAG	60
ACCGTGCTGC TGAGCACCGT GTTCAGCATC AGCCTGCTGA ACAACGAGGT GATCAAGGCC	120
GAGCAGCTGA ACATCAACAG CCAGAGCAAG TACACCAACC TCCAGAACCT GAAGATCACC	180
GACAAGGTGG AGGACTTCAA GGAGGACAAG GAGAAGGCCA AGGAGTGGGG CAAGGAGAAG	240
GAGAAGGAGT GGAAGCTTAC CGCCACCGAG AAGGGCAAGA TGAACAACCTT CCTGGACAAC	300
AAGAACGACA TCAAGACCAA CTACAAGGAG ATCACCTTCA GCATAGCCGG CAGCTTCGAG	360
GACGAGATCA AGGACCTGAA GGAGATCGAC AAGATGTTTCG ACAAGACCAA CCTGAGCAAC	420
AGCATCATCA CCTACAAGAA CGTGGAGCCC ACCACCATCG GCTTCAACAA GAGCCTGACC	480
GAGGGCAACA CCATCAACAG CGACGCCATG GCCCAGTTCA AGGAGCAGTT CCTGGACCGC	540
GACATCAAGT TCGACAGCTA CCTGGACACC CACCTGACCG CCCAGCAGGT GAGCAGCAAG	600
GAGCGCGTGA TCCTGAAGGT GACCGTCCCC AGCGGCAAGG GCAGCACCAC CCCCACCAAG	660
GCCGGCGTGA TCCTGAACAA CAGCGAGTAC AAGATGCTGA TCGACAACGG CTACATGGTG	720
CACGTGGACA AGGTGAGCAA GGTGGTGAAG AAGGGCGTGG AGTGCCTCCA GATCGAGGGC	780
ACCCTGAAGA AGAGTCTAGA CTTCAAGAAC GACATCAACG CCGAGGCCCA CAGCTGGGGC	840
ATGAAGAACT ACGAGGAGTG GGCCAAGGAC CTGACCGACA GCCAGCGCGA GGCCCTGGAC	900
GGCTACGCCC GCCAGGACTA CAAGGAGATC AACAACCTACC TGCGCAACCA GGGCGGCAGC	960
GGCAACGAGA AGCTGGACGC CCAGATCAAG AACATCAGCG ACGCCCTGGG CAAGAAGCCC	1020
ATCCCCGAGA ACATCACCGT GTACCGCTGG TGCGGCATGC CCGAGTTCGG CTACCAGATC	1080
AGCGACCCCC TGCCAGCCT GAAGGACTTC GAGGAGCAGT TCCTGAACAC CATCAAGGAG	1140

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GACAAGGGCT ACATGAGCAC CAGCCTGAGC AGCGAGCGCC TGGCCGCCTT CGGCAGCCGC 1200
 AAGATCATOC TGCGCCTGCA GGTGCCCAAG GGCAGCACTG GTGCCTACCT GAGCGCCATC 1260
 GGCGGCTTCG CCAGCGAGAA GGAGATCCTG CTGGATAAGG ACAGCAAGTA CCACATGAC 1320
 AAGGTGACCG AGGTGATCAT CAAGGGCGTG AAGCGCTACG TGGTGGACGC CACCTGCTG 1380
 ACCAACTAG 1389

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 9..2375
- (D) OTHER INFORMATION: /note= "Native DNA sequence encoding VIP3A(a) protein from AB88 as contained in pCIB7104"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGATGAAC ATG AAC AAG AAT AAT ACT AAA TTA AGC ACA AGA GCC TTA CCA 50
 Met Asn Lys Asn Asn Thr Lys Leu Ser Thr Arg Ala Leu Pro
 1 5 10

AGT TTT ATT GAT TAT TTT AAT GGC ATT TAT GGA TTT GCC ACT GGT ATC 98
 Ser Phe Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile
 15 20 25 30

AAA GAC ATT ATG AAC ATG ATT TTT AAA ACG GAT ACA GGT GGT GAT CTA 146
 Lys Asp Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asp Leu
 35 40 45

ACC CTA GAC GAA ATT TTA AAG AAT CAG CAG TTA CTA AAT GAT ATT TCT 194
 Thr Leu Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Asp Ile Ser
 50 55 60

GGT AAA TTG GAT GGG GTG AAT GGA AGC TTA AAT GAT CTT ATC GCA CAG 242
 Gly Lys Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln
 65 70 75

GGA AAC TTA AAT ACA GAA TTA TCT AAG GAA ATA TTA AAA ATT GCA AAT 290
 Gly Asn Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn
 80 85 90

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GAA CAA AAT CAA GTT TTA AAT GAT GTT AAT AAC AAA CTC GAT GCG ATA Glu Gln Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile 95 100 105 110	338
AAT ACG ATG CTT CGG GTA TAT CTA CCT AAA ATT ACC TCT ATG TTG AGT Asn Thr Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser 115 120 125	386
GAT GTA ATG AAA CAA AAT TAT GCG CTA AGT CTG CAA ATA GAA TAC TTA Asp Val Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu 130 135 140	434
AGT AAA CAA TTG CAA GAG ATT TCT GAT AAG TTG GAT ATT ATT AAT GTA Ser Lys Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val 145 150 155	482
AAT GTA CTT ATT AAC TCT ACA CTT ACT GAA ATT ACA CCT GCG TAT CAA Asn Val Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln 160 165 170	530
AGG ATT AAA TAT GTG AAC GAA AAA TTT GAG GAA TTA ACT TTT GCT ACA Arg Ile Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr 175 180 185 190	578
GAA ACT AGT TCA AAA GTA AAA AAG GAT GGC TCT CCT GCA GAT ATT CTT Glu Thr Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Leu 195 200 205	626
GAT GAG TTA ACT GAG TTA ACT GAA CTA GCG AAA AGT GTA ACA AAA AAT Asp Glu Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn 210 215 220	674
GAT GTG GAT GGT TTT GAA TTT TAC CTT AAT ACA TTC CAC GAT GTA ATG Asp Val Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met 225 230 235	722
GTA GGA AAT AAT TTA TTC GGG CGT TCA GCT TTA AAA ACT GCA TCG GAA Val Gly Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu 240 245 250	770
TTA ATT ACT AAA GAA AAT GTG AAA ACA AGT GGC AGT GAG GTC GGA AAT Leu Ile Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn 255 260 265 270	818
GTT TAT AAC TTC TTA ATT GTA TTA ACA GCT CTG CAA GCC CAA GCT TTT Val Tyr Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Gln Ala Phe 275 280 285	866
CTT ACT TTA ACA ACA TGC CGA AAA TTA TTA GGC TTA GCA GAT ATT GAT Leu Thr Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp 290 295 300	914
TAT ACT TCT ATT ATG AAT GAA CAT TTA AAT AAG GAA AAA GAG GAA TTT Tyr Thr Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe	962

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305	310	315	
AGA GTA AAC ATC CTC OCT ACA CTT TCT AAT ACT TTT TCT AAT CCT AAT			1010
Arg Val Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn			
320	325	330	
TAT GCA AAA GTT AAA GGA AGT GAT GAA GAT GCA AAG ATG ATT GTG GAA			1058
Tyr Ala Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu			
335	340	345	350
GCT AAA CCA GGA CAT GCA TTG ATT GGG TTT GAA ATT AGT AAT GAT TCA			1106
Ala Lys Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser			
355	360	365	
ATT ACA GTA TTA AAA GTA TAT GAG GCT AAG CTA AAA CAA AAT TAT CAA			1154
Ile Thr Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln			
370	375	380	
GTC GAT AAG GAT TCC TTA TCG GAA GTT ATT TAT GGT GAT ATG GAT AAA			1202
Val Asp Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys			
385	390	395	
TTA TTG TGC CCA GAT CAA TCT GAA CAA ATC TAT TAT ACA AAT AAC ATA			1250
Leu Leu Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile			
400	405	410	
GTA TTT CCA AAT GAA TAT GTA ATT ACT AAA ATT GAT TTC ACT AAA AAA			1298
Val Phe Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys			
415	420	425	430
ATG AAA ACT TTA AGA TAT GAG GTA ACA GCG AAT TTT TAT GAT TCT TCT			1346
Met Lys Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser			
435	440	445	
ACA GGA GAA ATT GAC TTA AAT AAG AAA AAA GTA GAA TCA AGT GAA GCG			1394
Thr Gly Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala			
450	455	460	
GAG TAT AGA ACG TTA AGT GCT AAT GAT GAT GGG GTG TAT ATG CCG TTA			1442
Glu Tyr Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu			
465	470	475	
GGT GTC ATC AGT GAA ACA TTT TTG ACT CCG ATT AAT GGG TTT GGC CTC			1490
Gly Val Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu			
480	485	490	
CAA GCT GAT GAA AAT TCA AGA TTA ATT ACT TTA ACA TGT AAA TCA TAT			1538
Gln Ala Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr			
495	500	505	510
TTA AGA GAA CTA CTG CTA GCA ACA GAC TTA AGC AAT AAA GAA ACT AAA			1586
Leu Arg Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys			
515	520	525	
TTG ATC GTC CCG CCA AGT GGT TTT ATT AGC AAT ATT GTA GAG AAC GGG			1634

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Leu	Ile	Val	Pro	Pro	Ser	Gly	Phe	Ile	Ser	Asn	Ile	Val	Glu	Asn	Gly	
			530					535					540			
TCC	ATA	GAA	GAG	GAC	AAT	TTA	GAG	CCG	TGG	AAA	GCA	AAT	AAT	AAG	AAT	1682
Ser	Ile	Glu	Glu	Asp	Asn	Leu	Glu	Pro	Trp	Lys	Ala	Asn	Asn	Lys	Asn	
		545					550					555				
GCG	TAT	GTA	GAT	CAT	ACA	GGC	GGA	GTG	AAT	GGA	ACT	AAA	GCT	TTA	TAT	1730
Ala	Tyr	Val	Asp	His	Thr	Gly	Gly	Val	Asn	Gly	Thr	Lys	Ala	Leu	Tyr	
	560					565					570					
GTT	CAT	AAG	GAC	GGA	GGA	ATT	TCA	CAA	TTT	ATT	GGA	GAT	AAG	TTA	AAA	1778
Val	His	Lys	Asp	Gly	Gly	Ile	Ser	Gln	Phe	Ile	Gly	Asp	Lys	Leu	Lys	
	575					580				585					590	
CCG	AAA	ACT	GAG	TAT	GTA	ATC	CAA	TAT	ACT	GTT	AAA	GGA	AAA	CCT	TCT	1826
Pro	Lys	Thr	Glu	Tyr	Val	Ile	Gln	Tyr	Thr	Val	Lys	Gly	Lys	Pro	Ser	
				595					600					605		
ATT	CAT	TTA	AAA	GAT	GAA	AAT	ACT	GGA	TAT	ATT	CAT	TAT	GAA	GAT	ACA	1874
Ile	His	Leu	Lys	Asp	Glu	Asn	Thr	Gly	Tyr	Ile	His	Tyr	Glu	Asp	Thr	
		610						615					620			
AAT	AAT	AAT	TTA	GAA	GAT	TAT	CAA	ACT	ATT	AAT	AAA	CGT	TTT	ACT	ACA	1922
Asn	Asn	Asn	Leu	Glu	Asp	Tyr	Gln	Thr	Ile	Asn	Lys	Arg	Phe	Thr	Thr	
		625					630					635				
GGA	ACT	GAT	TTA	AAG	GGA	GTG	TAT	TTA	ATT	TTA	AAA	AGT	CAA	AAT	GGA	1970
Gly	Thr	Asp	Leu	Lys	Gly	Val	Tyr	Leu	Ile	Leu	Lys	Ser	Gln	Asn	Gly	
	640					645					650					
GAT	GAA	GCT	TGG	GGA	GAT	AAC	TTT	ATT	ATT	TTG	GAA	ATT	AGT	CCT	TCT	2018
Asp	Glu	Ala	Trp	Gly	Asp	Asn	Phe	Ile	Ile	Leu	Glu	Ile	Ser	Pro	Ser	
	655				660					665					670	
GAA	AAG	TTA	TTA	AGT	CCA	GAA	TTA	ATT	AAT	ACA	AAT	AAT	TGG	ACG	AGT	2066
Glu	Lys	Leu	Leu	Ser	Pro	Glu	Leu	Ile	Asn	Thr	Asn	Asn	Trp	Thr	Ser	
				675					680					685		
ACG	GGA	TCA	ACT	AAT	ATT	AGC	GGT	AAT	ACA	CTC	ACT	CTT	TAT	CAG	GGA	2114
Thr	Gly	Ser	Thr	Asn	Ile	Ser	Gly	Asn	Thr	Leu	Thr	Leu	Tyr	Gln	Gly	
			690					695					700			
GGA	CGA	GGG	ATT	CTA	AAA	CAA	AAC	CTT	CAA	TTA	GAT	AGT	TTT	TCA	ACT	2162
Gly	Arg	Gly	Ile	Leu	Lys	Gln	Asn	Leu	Gln	Leu	Asp	Ser	Phe	Ser	Thr	
		705					710					715				
TAT	AGA	GTG	TAT	TTT	TCT	GTG	TCC	GGA	GAT	GCT	AAT	GTA	AGG	ATT	AGA	2210
Tyr	Arg	Val	Tyr	Phe	Ser	Val	Ser	Gly	Asp	Ala	Asn	Val	Arg	Ile	Arg	
	720					725					730					
AAT	TCT	AGG	GAA	GTG	TTA	TTT	GAA	AAA	AGA	TAT	ATG	AGC	GGT	GCT	AAA	2258
Asn	Ser	Arg	Glu	Val	Leu	Phe	Glu	Lys	Arg	Tyr	Met	Ser	Gly	Ala	Lys	
	735				740					745					750	

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GAT GTT TCT GAA ATG TTC ACT ACA AAA TTT GAG AAA GAT AAC TTT TAT	2306
Asp Val Ser Glu Met Phe Thr Thr Lys Phe Glu Lys Asp Asn Phe Tyr	
755 760 765	
ATA GAG CTT TCT CAA GGG AAT AAT TTA TAT GGT GGT CCT ATT GTA CAT	2354
Ile Glu Leu Ser Gln Gly Asn Asn Leu Tyr Gly Gly Pro Ile Val His	
770 775 780	
TTT TAC GAT GTC TCT ATT AAG TAA	2378
Phe Tyr Asp Val Ser Ile Lys	
785	

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Asn Lys Asn Asn Thr Lys Leu Ser Thr Arg Ala Leu Pro Ser Phe	
1 5 10 15	
Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp	
20 25 30	
Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asp Leu Thr Leu	
35 40 45	
Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Asp Ile Ser Gly Lys	
50 55 60	
Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn	
65 70 75 80	
Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln	
85 90 95	
Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Thr	
100 105 110	
Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val	
115 120 125	
Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys	
130 135 140	
Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val	
145 150 155 160	
Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile	

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165	170	175
Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr 180 185 190		
Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Leu Asp Glu 195 200 205		
Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val 210 215 220		
Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly 225 230 235 240		
Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile 245 250 255		
Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr 260 265 270		
Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Gln Ala Phe Leu Thr 275 280 285		
Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr 290 295 300		
Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val 305 310 315 320		
Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala 325 330 335		
Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys 340 345 350		
Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser Ile Thr 355 360 365		
Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp 370 375 380		
Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu 385 390 395 400		
Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe 405 410 415		
Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys 420 425 430		
Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly 435 440 445		
Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr 450 455 460		

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Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val
 465 470 475 480
 Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala
 485 490 495
 Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg
 500 505 510
 Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile
 515 520 525
 Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile
 530 535 540
 Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr
 545 550 555 560
 Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His
 565 570 575
 Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys
 580 585 590
 Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His
 595 600 605
 Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn
 610 615 620
 Asn Leu Glu Asp Tyr Gln Thr Ile Asn Lys Arg Phe Thr Thr Gly Thr
 625 630 635 640
 Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu
 645 650 655
 Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile Ser Pro Ser Glu Lys
 660 665 670
 Leu Leu Ser Pro Glu Leu Ile Asn Thr Asn Asn Trp Thr Ser Thr Gly
 675 680 685
 Ser Thr Asn Ile Ser Gly Asn Thr Leu Thr Leu Tyr Gln Gly Gly Arg
 690 695 700
 Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Ser Phe Ser Thr Tyr Arg
 705 710 715 720
 Val Tyr Phe Ser Val Ser Gly Asp Ala Asn Val Arg Ile Arg Asn Ser
 725 730 735
 Arg Glu Val Leu Phe Glu Lys Arg Tyr Met Ser Gly Ala Lys Asp Val
 740 745 750

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Ser Glu Met Phe Thr Thr Lys Phe Glu Lys Asp Asn Phe Tyr Ile Glu
755 760 765

Leu Ser Gln Gly Asn Asn Leu Tyr Gly Gly Pro Ile Val His Phe Tyr
770 775 780

Asp Val Ser Ile Lys
785

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 11..2389
- (D) OTHER INFORMATION: /note= "maize optimized DNA sequence encoding VIP3A(a)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

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GGATCCACCA ATGAACATGA ACAAGAACAA CACCAAGCTG AGCACCOCGG CCTGCOGAG      60
CTTCATCGAC TACTTCAACG GCATCTACGG CTTGCGCACC GGCATCAAGG ACATCATGAA      120
CATGATCTTC AAGACOGACA CCGGCGGOGA CCTGACCCTG GACGAGATCC TGAAGAACCA      180
GCAGCTGCTG AACGACATCA GCGGCAAGCT GGACGGCGTG AACGGCAGCC TGAACGACCT      240
GATCGCCCAG GGCAACCTGA ACACOGAGCT GAGCAAGGAG ATCCTTAAGA TCGCCAACGA      300
GCAGAACCAG GTGCTGAACG ACGTGAACAA CAAGCTGGAC GCCATCAACA CCATGCTGCG      360
CGTGTACCTG CGAAGATCA CCAGCATGCT GAGCGACGTG ATGAAGCAGA ACTACGCCCT      420
GAGCCTGCAG ATCGAGTACC TGAGCAAGCA GCTGCAGGAG ATCAGCGACA AGCTGGACAT      480
CATCAACGTG AACGTCTTGA TCAACAGCAC CCTGACCAGG ATCACCCCGG CCTACCAGCG      540
CATCAAGTAC GTGAACGAGA AGTTGGAAGA GCTGACCTTC GCCACOGAGA CCAGCAGCAA      600
GGTGAAGAAG GACGGCAGCC CGGCCGACAT CCTGGACGAG CTGACOGAGC TGACOGAGCT      660
GGCCAAGAGC GTGACCAAGA ACGACGTGGA CGGCTTCGAG TTCTACCTGA ACACCTTCCA      720

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CGACGTGATG	GTGGGCAACA	ACCTGTTCCG	CCGCAGCGCC	CTGAAGACCG	CCAGCGAGCT	780
GATCACCAAG	GAGAACGTGA	AGACCAGCGG	CAGCGAGGTG	GGCAACGTGT	ACAAC TTCCT	840
GATCGTGCTG	ACCGCCCTGC	AGGCCCAGGC	CTTCCTGACC	CTGACCACCT	GTCGCAAGCT	900
GCTGGGCCTG	GCGACATCG	ACTACACCAG	CATCATGAAC	GAGCACTTGA	ACAAGGAGAA	960
GGAGGAGTTC	CGCGTGAACA	TCCTGCCGAC	CCTGAGCAAC	ACCTTCAGCA	ACCCGAACTA	1020
CGCCAAGGTG	AAGGGCAGCG	ACGAGGACGC	CAAGATGATC	GTGGAGGCTA	AGCCGGGCCA	1080
CGCGTTGATC	GGCTTCGAGA	TCAGCAACGA	CAGCATCACC	GTGCTGAAGG	TGTACGAGGC	1140
CAAGCTGAAG	CAGAACTACC	AGGTGGACAA	GGACAGCTTG	AGCGAGGTGA	TCTACGGOGA	1200
CATGGACAAG	CTGCTGTGTC	CGGACCAGAG	CGAGCAAATC	TACTACACCA	ACAACATCGT	1260
GTTCCCGAAC	GAGTAOGTGA	TCACCAAGAT	CGACTTCACC	AAGAAGATGA	AGACCCTGCG	1320
CTACGAGGTG	ACCGCCAACT	TCTACGACAG	CAGCACCGGC	GAGATCGACC	TGAACAAGAA	1380
GAAGGTGGAG	AGCAGOGAGG	COGASTACOG	CACCTTGAGC	GCGAACGAOG	AOGGCGTCTA	1440
CATGCCACTG	GGCGTGATCA	GCGAGACCTT	CCTGACCCCG	ATCAACGGGT	TTGGCCTGCA	1500
GGCCGACGAG	AACAGCOGCC	TGATCACCCCT	GACCTGTAAG	AGCTACCTGC	GCGAGCTGCT	1560
GCTAGCCACC	GACCTGAGCA	ACAAGGAGAC	CAAGCTGATC	GTGCCACCGA	GOGGCTTCAT	1620
CAGCAACATC	GTGGAGAACG	GCAGCATCGA	GGAGGACAAC	CTGGAGCCGT	GGAAGGCCAA	1680
CAACAAGAAC	GCCTACGTGG	ACCACACCGG	CGGCGTGAAC	GGCACCAAGG	CCCTGTACGT	1740
GCACAAGGAC	GGGGGCATCA	GCCAGTTCAT	OGGOGACAAG	CTGAAGCCGA	AGACCGAGTA	1800
CGTGATCCAG	TACACCGTGA	AGGGCAAGCC	ATCGATTAC	CTGAAGGACG	AGAACAACCG	1860
CTACATCCAC	TACGAGGACA	CCAACAACAA	CCTGGAGGAC	TACCAGACCA	TCAACAAGCG	1920
CTTCACCACC	GGCACCGACC	TGAAGGGCGT	GTACCTGATC	CTGAAGAGCC	AGAACGGCGA	1980
CGAGGCCTGG	GGGACAACT	TCATCATCCT	GGAGATCAGC	COGAGCGAGA	AGCTGCTGAG	2040
CCCGGAGCTG	ATCAACACCA	ACAAC TGAC	CAGCACCGGC	AGCACCAACA	TCAGCGGCAA	2100
CACCCTGACC	CTGTACCAGG	GCGGCGCGG	CATCCTGAAG	CAGAACCTGC	AGCTGGACAG	2160
CTTCAGCACC	TACCGCGTGT	ACTTCAGOGT	GAGCGGGGAC	GCCAACGTGC	GCATCCGCAA	2220
CAGCGCGGAG	GTGCTGTTGG	AGAAGAGGTA	CATGAGCGGC	GCCAAGGACG	TGAGCGAGAT	2280
GTTCAACCACC	AAGTTCGAGA	AGGACAACCT	CTACATCGAG	CTGAGCCAGG	GCAACAACCT	2340

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GTACGGCGGC CCGATCGTGC ACTTCTACGA CGTGAGCATC AAGTTAACGT AGAGCTCAGA 2400
TCT 2403

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2612 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 118..2484
- (D) OTHER INFORMATION: /note= "Native DNA sequence encoding VIP3A(b) from AB424"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATTGAAATTG ATAAAAAGTT ATGAGTGTTC AATAATCAGT AATTACCAAT AAAGAATTAA 60
GAATACAAGT TTACAAGAAA TAAGTGTTAC AAAAAATAGC TGAAAAGGAA GATGAAC 117
ATG AAC AAG AAT AAT ACT AAA TTA AGC ACA AGA GCC TTA CCA AGT TTT 165
Met Asn Lys Asn Asn Thr Lys Leu Ser Thr Arg Ala Leu Pro Ser Phe
790 795 800 805
ATT GAT TAT TTC AAT GGC ATT TAT GGA TTT GCC ACT GGT ATC AAA GAC 213
Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp
810 815 820
ATT ATG AAC ATG ATT TTT AAA ACG GAT ACA GGT GGT GAT CTA ACC CTA 261
Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asp Leu Thr Leu
825 830 835
GAC GAA ATT TTA AAG AAT CAG CAG CTA CTA AAT GAT ATT TCT GGT AAA 309
Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Asp Ile Ser Gly Lys
840 845 850
TTG GAT GGG GTG AAT GGA AGC TTA AAT GAT CTT ATC GCA CAG GGA AAC 357
Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn
855 860 865
TTA AAT ACA GAA TTA TCT AAG GAA ATA TTA AAA ATT GCA AAT GAA CAA 405
Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln
870 875 880 885
AAT CAA GTT TTA AAT GAT GTT AAT AAC AAA CTC GAT GCG ATA AAT ACG 453

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Asn	Gln	Val	Leu	Asn	Asp	Val	Asn	Asn	Lys	Leu	Asp	Ala	Ile	Asn	Thr	
			890						895					900		
ATG	CTT	CGG	GTA	TAT	CTA	CCT	AAA	ATT	ACC	TCT	ATG	TTG	AGT	GAT	GTA	501
Met	Leu	Arg	Val	Tyr	Leu	Pro	Lys	Ile	Thr	Ser	Met	Leu	Ser	Asp	Val	
			905					910					915			
ATG	AAA	CAA	AAT	TAT	GCG	CTA	AGT	CTG	CAA	ATA	GAA	TAC	TTA	AGT	AAA	549
Met	Lys	Gln	Asn	Tyr	Ala	Leu	Ser	Leu	Gln	Ile	Glu	Tyr	Leu	Ser	Lys	
			920				925					930				
CAA	TTG	CAA	GAG	ATT	TCT	GAT	AAG	TTG	GAT	ATT	ATT	AAT	GTA	AAT	GTA	597
Gln	Leu	Gln	Glu	Ile	Ser	Asp	Lys	Leu	Asp	Ile	Ile	Asn	Val	Asn	Val	
			935				940					945				
CTT	ATT	AAC	TCT	ACA	CTT	ACT	GAA	ATT	ACA	CCT	GCG	TAT	CAA	AGG	ATT	645
Leu	Ile	Asn	Ser	Thr	Leu	Thr	Glu	Ile	Thr	Pro	Ala	Tyr	Gln	Arg	Ile	
						955				960					965	
AAA	TAT	GTG	AAC	GAA	AAA	TTT	GAG	GAA	TTA	ACT	TTT	GCT	ACA	GAA	ACT	693
Lys	Tyr	Val	Asn	Glu	Lys	Phe	Glu	Glu	Leu	Thr	Phe	Ala	Thr	Glu	Thr	
						970			975						980	
AGT	TCA	AAA	GTA	AAA	AAG	GAT	GGC	TCT	CCT	GCA	GAT	ATT	CGT	GAT	GAG	741
Ser	Ser	Lys	Val	Lys	Lys	Asp	Gly	Ser	Pro	Ala	Asp	Ile	Arg	Asp	Glu	
						985			990						995	
TTA	ACT	GAG	TTA	ACT	GAA	CTA	GCG	AAA	AGT	GTA	ACA	AAA	AAT	GAT	GTG	789
Leu	Thr	Glu	Leu	Thr	Glu	Leu	Ala	Lys	Ser	Val	Thr	Lys	Asn	Asp	Val	
			1000					1005					1010			
GAT	GGT	TTT	GAA	TTT	TAC	CTT	AAT	ACA	TTC	CAC	GAT	GTA	ATG	GTA	GGA	837
Asp	Gly	Phe	Glu	Phe	Tyr	Leu	Asn	Thr	Phe	His	Asp	Val	Met	Val	Gly	
			1015					1020				1025				
AAT	AAT	TTA	TTC	GGG	CGT	TCA	GCT	TTA	AAA	ACT	GCA	TCG	GAA	TTA	ATT	885
Asn	Asn	Leu	Phe	Gly	Arg	Ser	Ala	Leu	Lys	Thr	Ala	Ser	Glu	Leu	Ile	
						1030		1035			1040				1045	
ACT	AAA	GAA	AAT	GTG	AAA	ACA	AGT	GGC	AGT	GAG	GTC	GGA	AAT	GTT	TAT	933
Thr	Lys	Glu	Asn	Val	Lys	Thr	Ser	Gly	Ser	Glu	Val	Gly	Asn	Val	Tyr	
						1050			1055						1060	
AAC	TTC	CTA	ATT	GTA	TTA	ACA	GCT	CTG	CAA	GCA	AAA	GCT	TTT	CTT	ACT	981
Asn	Phe	Leu	Ile	Val	Leu	Thr	Ala	Leu	Gln	Ala	Lys	Ala	Phe	Leu	Thr	
						1065			1070						1075	
TTA	ACA	CCA	TGC	CGA	AAA	TTA	TTA	GGC	TTA	GCA	GAT	ATT	GAT	TAT	ACT	1029
Leu	Thr	Pro	Cys	Arg	Lys	Leu	Leu	Gly	Leu	Ala	Asp	Ile	Asp	Tyr	Thr	
						1080			1085				1090			
TCT	ATT	ATG	AAT	GAA	CAT	TTA	AAT	AAG	GAA	AAA	GAG	GAA	TTT	AGA	GTA	1077
Ser	Ile	Met	Asn	Glu	His	Leu	Asn	Lys	Glu	Lys	Glu	Glu	Phe	Arg	Val	
						1095			1100				1105			

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AAC ATC CTC CCT ACA CTT TCT AAT ACT TTT TCT AAT CCT AAT TAT GCA Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala 1110 1115 1120 1125	1125
AAA GTT AAA GGA AGT GAT GAA GAT GCA AAG ATG ATT GTG GAA GCT AAA Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys 1130 1135 1140	1173
CCA GGA CAT GCA TTG ATT GGG TTT GAA ATT AGT AAT GAT TCA ATT ACA Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser Ile Thr 1145 1150 1155	1221
GTA TTA AAA GTA TAT GAG GCT AAG CTA AAA CAA AAT TAT CAA GTC GAT Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp 1160 1165 1170	1269
AAG GAT TCC TTA TCG GAA GTT ATT TAT GGC GAT ATG GAT AAA TTA TTG Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu 1175 1180 1185	1317
TGC CCA GAT CAA TCT GGA CAA ATC TAT TAT ACA AAT AAC ATA GTA TTT Cys Pro Asp Gln Ser Gly Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe 1190 1195 1200 1205	1365
CCA AAT GAA TAT GTA ATT ACT AAA ATT GAT TTC ACT AAA AAA ATG AAA Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys 1210 1215 1220	1413
ACT TTA AGA TAT GAG GTA ACA GCG AAT TTT TAT GAT TCT TCT ACA GGA Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly 1225 1230 1235	1461
GAA ATT GAC TTA AAT AAG AAA AAA GTA GAA TCA AGT GAA GCG GAG TAT Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr 1240 1245 1250	1509
AGA ACG TTA AGT GCT AAT GAT GAT GGG GTG TAT ATG CCG TTA GGT GTC Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val 1255 1260 1265	1557
ATC AGT GAA ACA TTT TTG ACT CCG ATT AAT GGG TTT GGC CTC CAA GCT Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala 1270 1275 1280 1285	1605
GAT GAA AAT TCA AGA TTA ATT ACT TTA ACA TGT AAA TCA TAT TTA AGA Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg 1290 1295 1300	1653
GAA CTA CTG CTA GCA ACA GAC TTA AGC AAT AAA GAA ACT AAA TTG ATC Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile 1305 1310 1315	1701
GTC CCG CCA AGT GGT TTT ATT AGC AAT ATT GTA GAG AAC GGG TCC ATA Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile 1320 1325 1330	1749

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GAA GAG GAC AAT TTA GAG CCG TGG AAA GCA AAT AAT AAG AAT GCG TAT Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr 1335 1340 1345	1797
GTA GAT CAT ACA GGC GGA GTG AAT GGA ACT AAA GCT TTA TAT GTT CAT Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His 1350 1355 1360 1365	1845
AAG GAC GGA GGA ATT TCA CAA TTT ATT GGA GAT AAG TTA AAA CCG AAA Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys 1370 1375 1380	1893
ACT GAG TAT GTA ATC CAA TAT ACT GTT AAA GGA AAA CCT TCT ATT CAT Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His 1385 1390 1395	1941
TTA AAA GAT GAA AAT ACT GGA TAT ATT CAT TAT GAA GAT ACA AAT AAT Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn 1400 1405 1410	1989
AAT TTA GAA GAT TAT CAA ACT ATT AAT AAA CGT TTT ACT ACA GGA ACT Asn Leu Glu Asp Tyr Gln Thr Ile Asn Lys Arg Phe Thr Thr Gly Thr 1415 1420 1425	2037
GAT TTA AAG GGA GTG TAT TTA ATT TTA AAA AGT CAA AAT GGA GAT GAA Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu 1430 1435 1440 1445	2085
GCT TGG GGA GAT AAC TTT ATT ATT TTG GAA ATT AGT CCT TCT GAA AAG Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile Ser Pro Ser Glu Lys 1450 1455 1460	2133
TTA TTA AGT CCA GAA TTA ATT AAT ACA AAT AAT TGG ACG AGT ACG GGA Leu Leu Ser Pro Glu Leu Ile Asn Thr Asn Asn Trp Thr Ser Thr Gly 1465 1470 1475	2181
TCA ACT AAT ATT AGC GGT AAT ACA CTC ACT CTT TAT CAG GGA GGA CGA Ser Thr Asn Ile Ser Gly Asn Thr Leu Thr Leu Tyr Gln Gly Gly Arg 1480 1485 1490	2229
GGG ATT CTA AAA CAA AAC CTT CAA TTA GAT AGT TTT TCA ACT TAT AGA Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Ser Phe Ser Thr Tyr Arg 1495 1500 1505	2277
GTG TAT TTC TCT GTG TCC GGA GAT GCT AAT GTA AGG ATT AGA AAT TCT Val Tyr Phe Ser Val Ser Gly Asp Ala Asn Val Arg Ile Arg Asn Ser 1510 1515 1520 1525	2325
AGG GAA GTG TTA TTT GAA AAA AGA TAT ATG AGC GGT GCT AAA GAT GTT Arg Glu Val Leu Phe Glu Lys Arg Tyr Met Ser Gly Ala Lys Asp Val 1530 1535 1540	2373
TCT GAA ATG TTC ACT ACA AAA TTT GAG AAA GAT AAC TTC TAT ATA GAG Ser Glu Met Phe Thr Thr Lys Phe Glu Lys Asp Asn Phe Tyr Ile Glu	2421

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1545	1550	1555	
CTT TCT CAA GGG AAT AAT TTA TAT GGT GGT CCT ATT GTA CAT TTT TAC			2469
Leu Ser Gln Gly Asn Asn Leu Tyr Gly Gly Pro Ile Val His Phe Tyr			
1560	1565	1570	
GAT GTC TCT ATT AAG TAAGATCGGG ATCTAATATT AACAGTTTTT AGAAGCTAAT			2524
Asp Val Ser Ile Lys			
1575			
TCTTGATATAA TGTCCTTGAT TATGGAAAAA CACAATTTTG TTTGCTAAGA TGTATATATA			2584
GCTCACTCAT TAAAAGGCAA TCAAGCTT			2612

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 789 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Asn	Lys	Asn	Asn	Thr	Lys	Leu	Ser	Thr	Arg	Ala	Leu	Pro	Ser	Phe
1				5					10					15	
Ile	Asp	Tyr	Phe	Asn	Gly	Ile	Tyr	Gly	Phe	Ala	Thr	Gly	Ile	Lys	Asp
	20						25						30		
Ile	Met	Asn	Met	Ile	Phe	Lys	Thr	Asp	Thr	Gly	Gly	Asp	Leu	Thr	Leu
	35					40						45			
Asp	Glu	Ile	Leu	Lys	Asn	Gln	Gln	Leu	Leu	Asn	Asp	Ile	Ser	Gly	Lys
	50				55					60					
Leu	Asp	Gly	Val	Asn	Gly	Ser	Leu	Asn	Asp	Leu	Ile	Ala	Gln	Gly	Asn
	65			70				75						80	
Leu	Asn	Thr	Glu	Leu	Ser	Lys	Glu	Ile	Leu	Lys	Ile	Ala	Asn	Glu	Gln
		85					90							95	
Asn	Gln	Val	Leu	Asn	Asp	Val	Asn	Asn	Lys	Leu	Asp	Ala	Ile	Asn	Thr
	100					105							110		
Met	Leu	Arg	Val	Tyr	Leu	Pro	Lys	Ile	Thr	Ser	Met	Leu	Ser	Asp	Val
	115					120					125				
Met	Lys	Gln	Asn	Tyr	Ala	Leu	Ser	Leu	Gln	Ile	Glu	Tyr	Leu	Ser	Lys
	130				135					140					
Gln	Leu	Gln	Glu	Ile	Ser	Asp	Lys	Leu	Asp	Ile	Ile	Asn	Val	Asn	Val
	145				150				155					160	

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Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile
 165 170 175
 Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr
 180 185 190
 Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Arg Asp Glu
 195 200 205
 Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val
 210 215 220
 Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly
 225 230 235 240
 Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile
 245 250 255
 Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr
 260 265 270
 Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Lys Ala Phe Leu Thr
 275 280 285
 Leu Thr Pro Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr
 290 295 300
 Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val
 305 310 315 320
 Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala
 325 330 335
 Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys
 340 345 350
 Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser Ile Thr
 355 360 365
 Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp
 370 375 380
 Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu
 385 390 395 400
 Cys Pro Asp Gln Ser Gly Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe
 405 410 415
 Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys
 420 425 430
 Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly
 435 440 445

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Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr
 450 455 460
 Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val
 465 470 475 480
 Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala
 485 490 495
 Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg
 500 505 510
 Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile
 515 520 525
 Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile
 530 535 540
 Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr
 545 550 555 560
 Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His
 565 570 575
 Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys
 580 585 590
 Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His
 595 600 605
 Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr Glu Asp Thr Asn Asn
 610 615 620
 Asn Leu Glu Asp Tyr Gln Thr Ile Asn Lys Arg Phe Thr Thr Gly Thr
 625 630 635 640
 Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser Gln Asn Gly Asp Glu
 645 650 655
 Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile Ser Pro Ser Glu Lys
 660 665 670
 Leu Leu Ser Pro Glu Leu Ile Asn Thr Asn Asn Trp Thr Ser Thr Gly
 675 680 685
 Ser Thr Asn Ile Ser Gly Asn Thr Leu Thr Leu Tyr Gln Gly Gly Arg
 690 695 700
 Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Ser Phe Ser Thr Tyr Arg
 705 710 715 720
 Val Tyr Phe Ser Val Ser Gly Asp Ala Asn Val Arg Ile Arg Asn Ser
 725 730 735
 Arg Glu Val Leu Phe Glu Lys Arg Tyr Met Ser Gly Ala Lys Asp Val

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	740		745		750
Ser	Glu	Met	Phe	Thr	Thr
	755			Lys	Phe
				Glu	Lys
				Asp	Asn
					Phe
					Tyr
					Ile
					Glu
Leu	Ser	Gln	Gly	Asn	Asn
	770			Leu	Tyr
				Gly	Gly
				Pro	Ile
					Val
					His
					Phe
					Tyr
Asp	Val	Ser	Ile	Lys	
785					

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "forward primer used to make pCIB5526"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGATCCACCA TGAAGACCAA CCAGATCAGC

30

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "reverse primer used to make pCIB5526"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAGCTTCAGC TCCTT

15

(2) INFORMATION FOR SEQ ID NO:35:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 9..2564
 (D) OTHER INFORMATION: /note= "Maize optimized sequence encoding VIP1A(a) with the Bacillus secretion signal removed as contained in pCIB5526"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCCACC ATG AAG ACC AAC CAG ATC AGC ACC ACC CAG AAG AAC CAG CAG	50
Met Lys Thr Asn Gln Ile Ser Thr Thr Gln Lys Asn Gln Gln	
825 830 835	
AAG GAG ATG GAC CGC AAG GGC CTG CTG GGC TAC TAC TTC AAG GGC AAG	98
Lys Glu Met Asp Arg Lys Gly Leu Leu Gly Tyr Tyr Phe Lys Gly Lys	
840 845 850	
GAC TTC AGC AAC CTG ACC ATG TTC GCC CCC ACG CGT GAC AGC ACC CTG	146
Asp Phe Ser Asn Leu Thr Met Phe Ala Pro Thr Arg Asp Ser Thr Leu	
855 860 865	
ATC TAC GAC CAG CAG ACC GCC AAC AAG CTG CTG GAC AAG AAG CAG CAG	194
Ile Tyr Asp Gln Gln Thr Ala Asn Lys Leu Leu Asp Lys Lys Gln Gln	
870 875 880	
GAG TAC CAG AGC ATC CGC TGG ATC GGC CTG ATC CAG AGC AAG GAG ACC	242
Glu Tyr Gln Ser Ile Arg Trp Ile Gly Leu Ile Gln Ser Lys Glu Thr	
885 890 895	
GGC GAC TTC ACC TTC AAC CTG AGC GAG GAC GAG CAG GCC ATC ATC GAG	290
Gly Asp Phe Thr Phe Asn Leu Ser Glu Asp Glu Gln Ala Ile Ile Glu	
900 905 910 915	
ATC AAC GGC AAG ATC ATC AGC AAC AAG GGC AAG GAG AAG CAG GTG GTG	338
Ile Asn Gly Lys Ile Ile Ser Asn Lys Gly Lys Glu Lys Gln Val Val	
920 925 930	
CAC CTG GAG AAG GGC AAG CTG GTG CCC ATC AAG ATC GAG TAC CAG AGC	386
His Leu Glu Lys Gly Lys Leu Val Pro Ile Lys Ile Glu Tyr Gln Ser	
935 940 945	
GAC ACC AAG TTC AAC ATC GAC AGC AAG ACC TTC AAG GAG CTG AAG CTT	434

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Asp Thr Lys Phe Asn Ile Asp Ser Lys Thr Phe Lys Glu Leu Lys Leu	
950 955 960	
TTC AAG ATC GAC AGC CAG AAC CAG CCC CAG CAG GTG CAG CAG GAC GAG	482
Phe Lys Ile Asp Ser Gln Asn Gln Pro Gln Gln Val Gln Gln Asp Glu	
965 970 975	
CTG CGC AAC CCC GAG TTC AAC AAG AAG GAG AGC CAG GAG TTC CTG GCC	530
Leu Arg Asn Pro Glu Phe Asn Lys Lys Glu Ser Gln Glu Phe Leu Ala	
980 985 990 995	
AAG CCC AGC AAG ATC AAC CTG TTC ACC CAG CAG ATG AAG CGC GAG ATC	578
Lys Pro Ser Lys Ile Asn Leu Phe Thr Gln Gln Met Lys Arg Glu Ile	
1000 1005 1010	
GAC GAG GAC ACC GAC ACC GAC GGC GAC AGC ATC CCC GAC CTG TGG GAG	626
Asp Glu Asp Thr Asp Thr Asp Gly Asp Ser Ile Pro Asp Leu Trp Glu	
1015 1020 1025	
GAG AAC GGC TAC ACC ATC CAG AAC CGC ATC GCC GTG AAG TGG GAC GAC	674
Glu Asn Gly Tyr Thr Ile Gln Asn Arg Ile Ala Val Lys Trp Asp Asp	
1030 1035 1040	
AGC CTG GCT AGC AAG GGC TAC ACC AAG TTC GTG AGC AAC CCC CTG GAG	722
Ser Leu Ala Ser Lys Gly Tyr Thr Lys Phe Val Ser Asn Pro Leu Glu	
1045 1050 1055	
AGC CAC ACC GTG GGC GAC CCC TAC ACC GAC TAC GAG AAG GCC GCC CGC	770
Ser His Thr Val Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ala Arg	
1060 1065 1070 1075	
GAC CTG GAC CTG AGC AAC GCC AAG GAG ACC TTC AAC CCC CTG GTG GCC	818
Asp Leu Asp Leu Ser Asn Ala Lys Glu Thr Phe Asn Pro Leu Val Ala	
1080 1085 1090	
GCC TTC CCC AGC GTG AAC GTG AGC ATG GAG AAG GTG ATC CTG AGC CCC	866
Ala Phe Pro Ser Val Asn Val Ser Met Glu Lys Val Ile Leu Ser Pro	
1095 1100 1105	
AAC GAG AAC CTG AGC AAC AGC GTG GAG AGC CAC TCG AGC ACC AAC TGG	914
Asn Glu Asn Leu Ser Asn Ser Val Glu Ser His Ser Ser Thr Asn Trp	
1110 1115 1120	
AGC TAC ACC AAC ACC GAG GGC GCC AGC GTG GAG GCC GGC ATC GGT CCC	962
Ser Tyr Thr Asn Thr Glu Gly Ala Ser Val Glu Ala Gly Ile Gly Pro	
1125 1130 1135	
AAG GGC ATC AGC TTC GGC GTG AGC GTG AAC TAC CAG CAC AGC GAG ACC	1010
Lys Gly Ile Ser Phe Gly Val Ser Val Asn Tyr Gln His Ser Glu Thr	
1140 1145 1150 1155	
GTG GCC CAG GAG TGG GGC ACC AGC ACC GGC AAC ACC AGC CAG TTC AAC	1058
Val Ala Gln Glu Trp Gly Thr Ser Thr Gly Asn Thr Ser Gln Phe Asn	
1160 1165 1170	

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ACC GCC AGC GCC GGC TAC CTG AAC GCC AAC GTG CGC TAC AAC AAC GTG Thr Ala Ser Ala Gly Tyr Leu Asn Ala Asn Val Arg Tyr Asn Asn Val 1175 1180 1185	1106
GGC ACC GGC GCC ATC TAC GAC GTG AAG CCC ACC ACC AGC TTC GTG CTG Gly Thr Gly Ala Ile Tyr Asp Val Lys Pro Thr Thr Ser Phe Val Leu 1190 1195 1200	1154
AAC AAC GAC ACC ATC GCC ACC ATC ACC GCC AAG TCG AAT TCC ACC GCC Asn Asn Asp Thr Ile Ala Thr Ile Thr Ala Lys Ser Asn Ser Thr Ala 1205 1210 1215	1202
CTG AAC ATC AGC CCC GGC GAG AGC TAC CCC AAG AAG GGC CAG AAC GGC Leu Asn Ile Ser Pro Gly Glu Ser Tyr Pro Lys Lys Gly Gln Asn Gly 1220 1225 1230 1235	1250
ATC GCC ATC ACC AGC ATG GAC GAC TTC AAC AGC CAC CCC ATC ACC CTG Ile Ala Ile Thr Ser Met Asp Asp Phe Asn Ser His Pro Ile Thr Leu 1240 1245 1250	1298
AAC AAG AAG CAG GTG GAC AAC CTG CTG AAC AAC AAG CCC ATG ATG CTG Asn Lys Lys Gln Val Asp Asn Leu Leu Asn Asn Lys Pro Met Met Leu 1255 1260 1265	1346
GAG ACC AAC CAG ACC GAC GGC GTC TAC AAG ATC AAG GAC ACC CAC GGC Glu Thr Asn Gln Thr Asp Gly Val Tyr Lys Ile Lys Asp Thr His Gly 1270 1275 1280	1394
AAC ATC GTG ACG GGC GGC GAG TGG AAC GGC GTG ATC CAG CAG ATC AAG Asn Ile Val Thr Gly Gly Glu Trp Asn Gly Val Ile Gln Gln Ile Lys 1285 1290 1295	1442
GCC AAG ACC GCC AGC ATC ATC GTC GAC GAC GGC GAG CGC GTG GCC GAG Ala Lys Thr Ala Ser Ile Ile Val Asp Asp Gly Glu Arg Val Ala Glu 1300 1305 1310 1315	1490
AAG CGC GTG GCC GCC AAG GAC TAC GAG AAC CCC GAG GAC AAG ACC CCC Lys Arg Val Ala Ala Lys Asp Tyr Glu Asn Pro Glu Asp Lys Thr Pro 1320 1325 1330	1538
AGC CTG ACC CTG AAG GAC GCC CTG AAG CTG AGC TAC CCC GAC GAG ATC Ser Leu Thr Leu Lys Asp Ala Leu Lys Leu Ser Tyr Pro Asp Glu Ile 1335 1340 1345	1586
AAG GAG ATC GAG GGC TTG CTG TAC TAC AAG AAC AAG CCC ATC TAC GAG Lys Glu Ile Glu Gly Leu Leu Tyr Tyr Lys Asn Lys Pro Ile Tyr Glu 1350 1355 1360	1634
AGC AGC GTG ATG ACC TAT CTA GAC GAG AAC ACC GCC AAG GAG GTG ACC Ser Ser Val Met Thr Tyr Leu Asp Glu Asn Thr Ala Lys Glu Val Thr 1365 1370 1375	1682
AAG CAG CTG AAC GAC ACC ACC GGC AAG TTC AAG GAC GTG AGC CAC CTG Lys Gln Leu Asn Asp Thr Thr Gly Lys Phe Lys Asp Val Ser His Leu 1380 1385 1390 1395	1730

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TAC GAC GTG AAG CTG ACC CCC AAG ATG AAC GTG ACC ATC AAG CTG AGC Tyr Asp Val Lys Leu Thr Pro Lys Met Asn Val Thr Ile Lys Leu Ser 1400 1405 1410	1778
ATC CTG TAC GAC AAC GCC GAG AGC AAC GAC AAC AGC ATC GGC AAG TGG Ile Leu Tyr Asp Asn Ala Glu Ser Asn Asp Asn Ser Ile Gly Lys Trp 1415 1420 1425	1826
ACC AAC ACC AAC ATC GTG AGC GGC GGC AAC AAC GGC AAG AAG CAG TAC Thr Asn Thr Asn Ile Val Ser Gly Gly Asn Asn Gly Lys Lys Gln Tyr 1430 1435 1440	1874
AGC AGC AAC AAC CCC GAC GCC AAC CTG ACC CTG AAC ACC GAC GCC CAG Ser Ser Asn Asn Pro Asp Ala Asn Leu Thr Leu Asn Thr Asp Ala Gln 1445 1450 1455	1922
GAG AAG CTG AAC AAG AAC CGC GAC TAC TAC ATC AGC CTG TAC ATG AAG Glu Lys Leu Asn Lys Asn Arg Asp Tyr Tyr Ile Ser Leu Tyr Met Lys 1460 1465 1470 1475	1970
AGC GAG AAG AAC ACC CAG TGC GAG ATC ACC ATC GAC GGC GAG ATA TAC Ser Glu Lys Asn Thr Gln Cys Glu Ile Thr Ile Asp Gly Glu Ile Tyr 1480 1485 1490	2018
CCC ATC ACC ACC AAG ACC GTG AAC GTG AAC AAG GAC AAC TAC AAG CGC Pro Ile Thr Thr Lys Thr Val Asn Val Asn Lys Asp Asn Tyr Lys Arg 1495 1500 1505	2066
CTG GAC ATC ATC GCC CAC AAC ATC AAG AGC AAC CCC ATC AGC AGC CTG Leu Asp Ile Ile Ala His Asn Ile Lys Ser Asn Pro Ile Ser Ser Leu 1510 1515 1520	2114
CAC ATC AAG ACC AAC GAC GAG ATC ACC CTG TTC TGG GAC GAC ATA TCG His Ile Lys Thr Asn Asp Glu Ile Thr Leu Phe Trp Asp Asp Ile Ser 1525 1530 1535	2162
ATT ACC GAC GTC GCC AGC ATC AAG CCC GAG AAC CTG ACC GAC AGC GAG Ile Thr Asp Val Ala Ser Ile Lys Pro Glu Asn Leu Thr Asp Ser Glu 1540 1545 1550 1555	2210
ATC AAG CAG ATA TAC AGT CGC TAC GGC ATC AAG CTG GAG GAC GGC ATC Ile Lys Gln Ile Tyr Ser Arg Tyr Gly Ile Lys Leu Glu Asp Gly Ile 1560 1565 1570	2258
CTG ATC GAC AAG AAA GGC GGC ATC CAC TAC GGC GAG TTC ATC AAC GAG Leu Ile Asp Lys Lys Gly Gly Ile His Tyr Gly Glu Phe Ile Asn Glu 1575 1580 1585	2306
GCC AGC TTC AAC ATC GAG CCC CTG CAG AAC TAC GTG ACC AAG TAC GAG Ala Ser Phe Asn Ile Glu Pro Leu Gln Asn Tyr Val Thr Lys Tyr Glu 1590 1595 1600	2354
GTG ACC TAC AGC AGC GAG CTG GGC CCC AAC GTG AGC GAC ACC CTG GAG Val Thr Tyr Ser Ser Glu Leu Gly Pro Asn Val Ser Asp Thr Leu Glu	2402

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1605	1610	1615	
AGC GAC AAG ATT TAC AAG GAC GGC ACC ATC AAG TTC GAC TTC ACC AAG			2450
Ser Asp Lys Ile Tyr Lys Asp Gly Thr Ile Lys Phe Asp Phe Thr Lys			
1620	1625	1630	1635
TAC AGC AAG AAC GAG CAG GGC CTG TTC TAC GAC AGC GGC CTG AAC TGG			2498
Tyr Ser Lys Asn Glu Gln Gly Leu Phe Tyr Asp Ser Gly Leu Asn Trp			
	1640	1645	1650
GAC TTC AAG ATC AAC GCC ATC ACC TAC GAC GGC AAG GAG ATG AAC GTG			2546
Asp Phe Lys Ile Asn Ala Ile Thr Tyr Asp Gly Lys Glu Met Asn Val			
	1655	1660	1665
TTC CAC CGC TAC AAC AAG TAGATCTGAG CT			2576
Phe His Arg Tyr Asn Lys			
1670			

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Lys	Thr	Asn	Gln	Ile	Ser	Thr	Thr	Gln	Lys	Asn	Gln	Gln	Lys	Glu
1				5					10					15	
Met	Asp	Arg	Lys	Gly	Leu	Leu	Gly	Tyr	Tyr	Phe	Lys	Gly	Lys	Asp	Phe
	20						25						30		
Ser	Asn	Leu	Thr	Met	Phe	Ala	Pro	Thr	Arg	Asp	Ser	Thr	Leu	Ile	Tyr
	35						40					45			
Asp	Gln	Gln	Thr	Ala	Asn	Lys	Leu	Leu	Asp	Lys	Lys	Gln	Gln	Glu	Tyr
	50					55				60					
Gln	Ser	Ile	Arg	Trp	Ile	Gly	Leu	Ile	Gln	Ser	Lys	Glu	Thr	Gly	Asp
65				70					75					80	
Phe	Thr	Phe	Asn	Leu	Ser	Glu	Asp	Glu	Gln	Ala	Ile	Ile	Glu	Ile	Asn
			85					90					95		
Gly	Lys	Ile	Ile	Ser	Asn	Lys	Gly	Lys	Glu	Lys	Gln	Val	Val	His	Leu
		100					105					110			
Glu	Lys	Gly	Lys	Leu	Val	Pro	Ile	Lys	Ile	Glu	Tyr	Gln	Ser	Asp	Thr
	115					120					125				
Lys	Phe	Asn	Ile	Asp	Ser	Lys	Thr	Phe	Lys	Glu	Leu	Lys	Leu	Phe	Lys

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130		135		140
Ile Asp Ser Gln Asn Gln Pro Gln Gln Val Gln Gln Asp Glu Leu Arg				
145		150		155
Asn Pro Glu Phe Asn Lys Lys Glu Ser Gln Glu Phe Leu Ala Lys Pro				
	165		170	175
Ser Lys Ile Asn Leu Phe Thr Gln Gln Met Lys Arg Glu Ile Asp Glu				
	180		185	190
Asp Thr Asp Thr Asp Gly Asp Ser Ile Pro Asp Leu Trp Glu Glu Asn				
	195		200	205
Gly Tyr Thr Ile Gln Asn Arg Ile Ala Val Lys Trp Asp Asp Ser Leu				
	210		215	220
Ala Ser Lys Gly Tyr Thr Lys Phe Val Ser Asn Pro Leu Glu Ser His				
	225		230	235
Thr Val Gly Asp Pro Tyr Thr Asp Tyr Glu Lys Ala Ala Arg Asp Leu				
	245		250	255
Asp Leu Ser Asn Ala Lys Glu Thr Phe Asn Pro Leu Val Ala Ala Phe				
	260		265	270
Pro Ser Val Asn Val Ser Met Glu Lys Val Ile Leu Ser Pro Asn Glu				
	275		280	285
Asn Leu Ser Asn Ser Val Glu Ser His Ser Ser Thr Asn Trp Ser Tyr				
	290		295	300
Thr Asn Thr Glu Gly Ala Ser Val Glu Ala Gly Ile Gly Pro Lys Gly				
	305		310	315
Ile Ser Phe Gly Val Ser Val Asn Tyr Gln His Ser Glu Thr Val Ala				
	325		330	335
Gln Glu Trp Gly Thr Ser Thr Gly Asn Thr Ser Gln Phe Asn Thr Ala				
	340		345	350
Ser Ala Gly Tyr Leu Asn Ala Asn Val Arg Tyr Asn Asn Val Gly Thr				
	355		360	365
Gly Ala Ile Tyr Asp Val Lys Pro Thr Thr Ser Phe Val Leu Asn Asn				
	370		375	380
Asp Thr Ile Ala Thr Ile Thr Ala Lys Ser Asn Ser Thr Ala Leu Asn				
	385		390	395
Ile Ser Pro Gly Glu Ser Tyr Pro Lys Lys Gly Gln Asn Gly Ile Ala				
	405		410	415
Ile Thr Ser Met Asp Asp Phe Asn Ser His Pro Ile Thr Leu Asn Lys				
	420		425	430

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Lys Gln Val Asp Asn Leu Leu Asn Asn Lys Pro Met Met Leu Glu Thr
 435 440 445
 Asn Gln Thr Asp Gly Val Tyr Lys Ile Lys Asp Thr His Gly Asn Ile
 450 455 460
 Val Thr Gly Gly Glu Trp Asn Gly Val Ile Gln Gln Ile Lys Ala Lys
 465 470 475 480
 Thr Ala Ser Ile Ile Val Asp Asp Gly Glu Arg Val Ala Glu Lys Arg
 485 490 495
 Val Ala Ala Lys Asp Tyr Glu Asn Pro Glu Asp Lys Thr Pro Ser Leu
 500 505 510
 Thr Leu Lys Asp Ala Leu Lys Leu Ser Tyr Pro Asp Glu Ile Lys Glu
 515 520 525
 Ile Glu Gly Leu Leu Tyr Tyr Lys Asn Lys Pro Ile Tyr Glu Ser Ser
 530 535 540
 Val Met Thr Tyr Leu Asp Glu Asn Thr Ala Lys Glu Val Thr Lys Gln
 545 550 555 560
 Leu Asn Asp Thr Thr Gly Lys Phe Lys Asp Val Ser His Leu Tyr Asp
 565 570 575
 Val Lys Leu Thr Pro Lys Met Asn Val Thr Ile Lys Leu Ser Ile Leu
 580 585 590
 Tyr Asp Asn Ala Glu Ser Asn Asp Asn Ser Ile Gly Lys Trp Thr Asn
 595 600 605
 Thr Asn Ile Val Ser Gly Gly Asn Asn Gly Lys Lys Gln Tyr Ser Ser
 610 615 620
 Asn Asn Pro Asp Ala Asn Leu Thr Leu Asn Thr Asp Ala Gln Glu Lys
 625 630 635 640
 Leu Asn Lys Asn Arg Asp Tyr Tyr Ile Ser Leu Tyr Met Lys Ser Glu
 645 650 655
 Lys Asn Thr Gln Cys Glu Ile Thr Ile Asp Gly Glu Ile Tyr Pro Ile
 660 665 670
 Thr Thr Lys Thr Val Asn Val Asn Lys Asp Asn Tyr Lys Arg Leu Asp
 675 680 685
 Ile Ile Ala His Asn Ile Lys Ser Asn Pro Ile Ser Ser Leu His Ile
 690 695 700
 Lys Thr Asn Asp Glu Ile Thr Leu Phe Trp Asp Asp Ile Ser Ile Thr
 705 710 715 720

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[illegible]

(2) INFORMATION FOR SEQ ID NO:37: ..

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "forward primer used to make pCIB5527"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGATCCACCA TGCTGCAGAA CCTGAAGATC AC

32

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "reverse primer used to make pCIB5527"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAGCTTCCAC TCCTTCTC

18

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 9..1238
 (D) OTHER INFORMATION: /note= "Maize optimized DNA sequence encoding VIP2A(a) with the Bacillus secretion signal removed as contained in pCIB5527"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATCCACC ATG CTG CAG AAC CTG AAG ATC ACC GAC AAG GTG GAG GAC TTC	50
Met Leu Gln Asn Leu Lys Ile Thr Asp Lys Val Glu Asp Phe	
855 860 865	
AAG GAG GAC AAG GAG AAG GCC AAG GAG TGG GGC AAG GAG AAG GAG AAG	98
Lys Glu Asp Lys Glu Lys Ala Lys Glu Trp Gly Lys Glu Lys Glu Lys	
870 875 880	
GAG TGG AAG CTT ACC GCC ACC GAG AAG GGC AAG ATG AAC AAC TTC CTG	146
Glu Trp Lys Leu Thr Ala Thr Glu Lys Gly Lys Met Asn Asn Phe Leu	
885 890 895	
GAC AAC AAG AAC GAC ATC AAG ACC AAC TAC AAG GAG ATC ACC TTC AGC	194
Asp Asn Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr Phe Ser	
900 905 910	
ATA GCC GGC AGC TTC GAG GAC GAG ATC AAG GAC CTG AAG GAG ATC GAC	242

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Ile Ala Gly Ser Phe Glu Asp Glu Ile Lys Asp Leu Lys Glu Ile Asp 915 920 925 930	
AAG ATG TTC GAC AAG ACC AAC CTG AGC AAC AGC ATC ATC ACC TAC AAG Lys Met Phe Asp Lys Thr Asn Leu Ser Asn Ser Ile Ile Thr Tyr Lys 935 940 945	290
AAC GTG GAG CCC ACC ACC ATC GGC TTC AAC AAG AGC CTG ACC GAG GGC Asn Val Glu Pro Thr Thr Ile Gly Phe Asn Lys Ser Leu Thr Glu Gly 950 955 960	338
AAC ACC ATC AAC AGC GAC GCC ATG GCC CAG TTC AAG GAG CAG TTC CTG Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln Phe Leu 965 970 975	386
GAC CGC GAC ATC AAG TTC GAC AGC TAC CTG GAC ACC CAC CTG ACC GCC Asp Arg Asp Ile Lys Phe Asp Ser Tyr Leu Asp Thr His Leu Thr Ala 980 985 990	434
CAG CAG GTG AGC AGC AAG GAG CGC GTG ATC CTG AAG GTG ACC GTC CCC Gln Gln Val Ser Ser Lys Glu Arg Val Ile Leu Lys Val Thr Val Pro 995 1000 1005 1010	482
AGC GGC AAG GGC AGC ACC ACC CCC ACC AAG GCC GGC GTG ATC CTG AAC Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile Leu Asn 1015 1020 1025	530
AAC AGC GAG TAC AAG ATG CTG ATC GAC AAC GGC TAC ATG GTG CAC GTG Asn Ser Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Met Val His Val 1030 1035 1040	578
GAC AAG GTG AGC AAG GTG GTG AAG AAG GGC GTG GAG TGC CTC CAG ATC Asp Lys Val Ser Lys Val Val Lys Lys Gly Val Glu Cys Leu Gln Ile 1045 1050 1055	626
GAG GGC ACC CTG AAG AAG AGT CTA GAC TTC AAG AAC GAC ATC AAC GCC Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile Asn Ala 1060 1065 1070	674
GAG GCC CAC AGC TGG GGC ATG AAG AAC TAC GAG GAG TGG GCC AAG GAC Glu Ala His Ser Trp Gly Met Lys Asn Tyr Glu Glu Trp Ala Lys Asp 1075 1080 1085 1090	722
CTG ACC GAC AGC CAG CGC GAG GCC CTG GAC GGC TAC GCC CGC CAG GAC Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg Gln Asp 1095 1100 1105	770
TAC AAG GAG ATC AAC AAC TAC CTG CGC AAC CAG GGC GGC AGC GGC AAC Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser Gly Asn 1110 1115 1120	818
GAG AAG CTG GAC GCC CAG ATC AAG AAC ATC AGC GAC GCC CTG GGC AAG Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala Leu Gly Lys 1125 1130 1135	866

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AAG CCC ATC CCC GAG AAC ATC ACC GTG TAC CGC TGG TGC GGC ATG CCC Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly Met Pro 1140 1145 1150	914
GAG TTC GGC TAC CAG ATC AGC GAC CCC CTG CCC AGC CTG AAG GAC TTC Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys Asp Phe 1155 1160 1165 1170	962
GAG GAG CAG TTC CTG AAC ACC ATC AAG GAG GAC AAG GGC TAC ATG AGC Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr Met Ser 1175 1180 1185	1010
ACC AGC CTG AGC AGC GAG CGC CTG GCC GCC TTC GGC AGC CGC AAG ATC Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg Lys Ile 1190 1195 1200	1058
ATC CTG CGC CTG CAG GTG CCC AAG GGC AGC ACT GGT GCC TAC CTG AGC Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr Leu Ser 1205 1210 1215	1106
GCC ATC GGC GGC TTC GCC AGC GAG AAG GAG ATC CTG CTG GAT AAG GAC Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp Lys Asp 1220 1225 1230	1154
AGC AAG TAC CAC ATC GAC AAG GTG ACC GAG GTG ATC ATC AAG GGC GTG Ser Lys Tyr His Ile Asp Lys Val Thr Glu Val Ile Ile Lys Gly Val 1235 1240 1245 1250	1202
AAG CGC TAC GTG GTG GAC GCC ACC CTG CTG ACC AAC TAG Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn 1255 1260	1241

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Leu Gln Asn Leu Lys Ile Thr Asp Lys Val Glu Asp Phe Lys Glu 1 5 10 15
Asp Lys Glu Lys Ala Lys Glu Trp Gly Lys Glu Lys Glu Lys Glu Trp 20 25 30
Lys Leu Thr Ala Thr Glu Lys Gly Lys Met Asn Asn Phe Leu Asp Asn 35 40 45
Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr Phe Ser Ile Ala 50 55 60

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Gly Ser Phe Glu Asp Glu Ile Lys Asp Leu Lys Glu Ile Asp Lys Met
 65 70 75 80
 Phe Asp Lys Thr Asn Leu Ser Asn Ser Ile Ile Thr Tyr Lys Asn Val
 85 90 95
 Glu Pro Thr Thr Ile Gly Phe Asn Lys Ser Leu Thr Glu Gly Asn Thr
 100 105 110
 Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln Phe Leu Asp Arg
 115 120 125
 Asp Ile Lys Phe Asp Ser Tyr Leu Asp Thr His Leu Thr Ala Gln Gln
 130 135 140
 Val Ser Ser Lys Glu Arg Val Ile Leu Lys Val Thr Val Pro Ser Gly
 145 150 155 160
 Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile Leu Asn Asn Ser
 165 170 175
 Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Met Val His Val Asp Lys
 180 185 190
 Val Ser Lys Val Val Lys Lys Gly Val Glu Cys Leu Gln Ile Glu Gly
 195 200 205
 Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile Asn Ala Glu Ala
 210 215 220
 His Ser Trp Gly Met Lys Asn Tyr Glu Glu Trp Ala Lys Asp Leu Thr
 225 230 235 240
 Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg Gln Asp Tyr Lys
 245 250 255
 Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser Gly Asn Glu Lys
 260 265 270
 Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala Leu Gly Lys Lys Pro
 275 280 285
 Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly Met Pro Glu Phe
 290 295 300
 Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys Asp Phe Glu Glu
 305 310 315 320
 Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr Met Ser Thr Ser
 325 330 335
 Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg Lys Ile Ile Leu
 340 345 350

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Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr Leu Ser Ala Ile
355 360 365

Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp Lys Asp Ser Lys
370 375 380

Tyr His Ile Asp Lys Val Thr Glu Val Ile Ile Lys Gly Val Lys Arg
385 390 395 400

Tyr Val Val Asp Ala Thr Leu Leu Thr Asn
405 410

(2) INFORMATION FOR SEO ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide encoding eukaryotic secretion signal used to construct pCIB5527"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEO ID NO:41:

GGATCCACCA TGGGCTGGAG CTGGATCTTC CTGTTCTGTC TGAGCGGCGC CGCGGGCGTG 60

CACTGCCTGC AG 72

(2) INFORMATION FOR SEO ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 9..1238
(D) OTHER INFORMATION: /note= "Maize optimized DNA
sequence encoding VIP2A(a) with the Bacillus secretion signal
removed and the eukaryotic secretion signal inserted as

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contained in pCIB5528"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCCACC ATG CTG CAG AAC CTG AAG ATC ACC GAC AAG GTG GAG GAC TTC	50
Met Leu Gln Asn Leu Lys Ile Thr Asp Lys Val Glu Asp Phe	
415 420	
AAG GAG GAC AAG GAG AAG GCC AAG GAG TGG GGC AAG GAG AAG GAG AAG	98
Lys Glu Asp Lys Glu Lys Ala Lys Glu Trp Gly Lys Glu Lys Glu Lys	
425 430 435 440	
GAG TGG AAG CTT ACC GCC ACC GAG AAG GGC AAG ATG AAC AAC TTC CTG	146
Glu Trp Lys Leu Thr Ala Thr Glu Lys Gly Lys Met Asn Asn Phe Leu	
445 450 455	
GAC AAC AAG AAC GAC ATC AAG ACC AAC TAC AAG GAG ATC ACC TTC AGC	194
Asp Asn Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr Phe Ser	
460 465 470	
ATA GCC GGC AGC TTC GAG GAC GAG ATC AAG GAC CTG AAG GAG ATC GAC	242
Ile Ala Gly Ser Phe Glu Asp Glu Ile Lys Asp Leu Lys Glu Ile Asp	
475 480 485	
AAG ATG TTC GAC AAG ACC AAC CTG AGC AAC AGC ATC ATC ACC TAC AAG	290
Lys Met Phe Asp Lys Thr Asn Leu Ser Asn Ser Ile Ile Thr Tyr Lys	
490 495 500	
AAC GTG GAG CCC ACC ACC ATC GGC TTC AAC AAG AGC CTG ACC GAG GGC	338
Asn Val Glu Pro Thr Thr Ile Gly Phe Asn Lys Ser Leu Thr Glu Gly	
505 510 515 520	
AAC ACC ATC AAC AGC GAC GCC ATG GCC CAG TTC AAG GAG CAG TTC CTG	386
Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln Phe Leu	
525 530 535	
GAC CGC GAC ATC AAG TTC GAC AGC TAC CTG GAC ACC CAC CTG ACC GCC	434
Asp Arg Asp Ile Lys Phe Asp Ser Tyr Leu Asp Thr His Leu Thr Ala	
540 545 550	
CAG CAG GTG AGC AGC AAG GAG CGC GTG ATC CTG AAG GTG ACC GTC CCC	482
Gln Gln Val Ser Ser Lys Glu Arg Val Ile Leu Lys Val Thr Val Pro	
555 560 565	
AGC GGC AAG GGC AGC ACC ACC CCC ACC AAG GCC GGC GTG ATC CTG AAC	530
Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile Leu Asn	
570 575 580	
AAC AGC GAG TAC AAG ATG CTG ATC GAC AAC GGC TAC ATG GTG CAC GTG	578
Asn Ser Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Met Val His Val	
585 590 595 600	
GAC AAG GTG AGC AAG GTG GTG AAG AAG GGC GTG GAG TGC CTC CAG ATC	626
Asp Lys Val Ser Lys Val Val Lys Lys Gly Val Glu Cys Leu Gln Ile	

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																605																	610																	615																																		
GAG	GGC	ACC	CTG	AAG	AAG	AGT	CTA	GAC	TTC	AAG	AAC	GAC	ATC	AAC	GCC		674																																																																			
Glu	Gly	Thr	Leu	Lys	Lys	Ser	Leu	Asp	Phe	Lys	Asn	Asp	Ile	Asn	Ala																																																																					
																620																	625																	630																																		
GAG	GCC	CAC	AGC	TGG	GGC	ATG	AAG	AAC	TAC	GAG	GAG	TGG	GCC	AAG	GAC		722																																																																			
Glu	Ala	His	Ser	Trp	Gly	Met	Lys	Asn	Tyr	Glu	Glu	Trp	Ala	Lys	Asp																																																																					
																635																	640																	645																																		
CTG	ACC	GAC	AGC	CAG	CGC	GAG	GCC	CTG	GAC	GGC	TAC	GCC	CGC	CAG	GAC		770																																																																			
Leu	Thr	Asp	Ser	Gln	Arg	Glu	Ala	Leu	Asp	Gly	Tyr	Ala	Arg	Gln	Asp																																																																					
																650																	655																	660																																		
TAC	AAG	GAG	ATC	AAC	AAC	TAC	CTG	CGC	AAC	CAG	GGC	GGC	AGC	GGC	AAC		818																																																																			
Tyr	Lys	Glu	Ile	Asn	Asn	Tyr	Leu	Arg	Asn	Gln	Gly	Gly	Ser	Gly	Asn																																																																					
																665																	670																	675																	680																	
GAG	AAG	CTG	GAC	GCC	CAG	ATC	AAG	AAC	ATC	AGC	GAC	GCC	CTG	GGC	AAG		866																																																																			
Glu	Lys	Leu	Asp	Ala	Gln	Ile	Lys	Asn	Ile	Ser	Asp	Ala	Leu	Gly	Lys																																																																					
																685																	690																	695																																		
AAG	CCC	ATC	CCC	GAG	AAC	ATC	ACC	GTG	TAC	CGC	TGG	TGC	GGC	ATG	CCC		914																																																																			
Lys	Pro	Ile	Pro	Glu	Asn	Ile	Thr	Val	Tyr	Arg	Trp	Cys	Gly	Met	Pro																																																																					
																700																	705																	710																																		
GAG	TTC	GGC	TAC	CAG	ATC	AGC	GAC	CCC	CTG	CCC	AGC	CTG	AAG	GAC	TTC		962																																																																			
Glu	Phe	Gly	Tyr	Gln	Ile	Ser	Asp	Pro	Leu	Pro	Ser	Leu	Lys	Asp	Phe																																																																					
																715																	720																	725																																		
GAG	GAG	CAG	TTC	CTG	AAC	ACC	ATC	AAG	GAG	GAC	AAG	GGC	TAC	ATG	AGC		1010																																																																			
Glu	Glu	Gln	Phe	Leu	Asn	Thr	Ile	Lys	Glu	Asp	Lys	Gly	Tyr	Met	Ser																																																																					
																730																	735																	740																																		
ACC	AGC	CTG	AGC	AGC	GAG	CGC	CTG	GCC	GCC	TTC	GGC	AGC	CGC	AAG	ATC		1058																																																																			
Thr	Ser	Leu	Ser	Ser	Glu	Arg	Leu	Ala	Ala	Phe	Gly	Ser	Arg	Lys	Ile																																																																					
																745																	750																	755																	760																	
ATC	CTG	CGC	CTG	CAG	GTG	CCC	AAG	GGC	AGC	ACT	GGT	GCC	TAC	CTG	AGC		1106																																																																			
Ile	Leu	Arg	Leu	Gln	Val	Pro	Lys	Gly	Ser	Thr	Gly	Ala	Tyr	Leu	Ser																																																																					
																765																	770																	775																																		
GCC	ATC	GGC	GGC	TTC	GCC	AGC	GAG	AAG	GAG	ATC	CTG	CTG	GAT	AAG	GAC		1154																																																																			
Ala	Ile	Gly	Gly	Phe	Ala	Ser	Glu	Lys	Glu	Ile	Leu	Leu	Asp	Lys	Asp																																																																					
																780																	785																	790																																		
AGC	AAG	TAC	CAC	ATC	GAC	AAG	GTG	ACC	GAG	GTG	ATC	ATC	AAG	GGC	GTG		1202																																																																			
Ser	Lys	Tyr	His	Ile	Asp	Lys	Val	Thr	Glu	Val	Ile	Ile	Lys	Gly	Val																																																																					
																795																	800																	805																																		
AAG	CGC	TAC	GTG	GTG	GAC	GCC	ACC	CTG	CTG	ACC	AAC	TAG						1241																																																																		
Lys	Arg	Tyr	Val	Val	Asp	Ala	Thr	Leu	Leu	Thr	Asn																																																																									
																810																	815																	820																																		

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(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

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Met Leu Gln Asn Leu Lys Ile Thr Asp Lys Val Glu Asp Phe Lys Glu
 1             5             10             15
Asp Lys Glu Lys Ala Lys Glu Trp Gly Lys Glu Lys Glu Lys Glu Trp
          20             25             30
Lys Leu Thr Ala Thr Glu Lys Gly Lys Met Asn Asn Phe Leu Asp Asn
          35             40             45
Lys Asn Asp Ile Lys Thr Asn Tyr Lys Glu Ile Thr Phe Ser Ile Ala
          50             55             60
Gly Ser Phe Glu Asp Glu Ile Lys Asp Leu Lys Glu Ile Asp Lys Met
          65             70             75             80
Phe Asp Lys Thr Asn Leu Ser Asn Ser Ile Ile Thr Tyr Lys Asn Val
          85             90             95
Glu Pro Thr Thr Ile Gly Phe Asn Lys Ser Leu Thr Glu Gly Asn Thr
          100            105            110
Ile Asn Ser Asp Ala Met Ala Gln Phe Lys Glu Gln Phe Leu Asp Arg
          115            120            125
Asp Ile Lys Phe Asp Ser Tyr Leu Asp Thr His Leu Thr Ala Gln Gln
          130            135            140
Val Ser Ser Lys Glu Arg Val Ile Leu Lys Val Thr Val Pro Ser Gly
          145            150            155            160
Lys Gly Ser Thr Thr Pro Thr Lys Ala Gly Val Ile Leu Asn Asn Ser
          165            170            175
Glu Tyr Lys Met Leu Ile Asp Asn Gly Tyr Met Val His Val Asp Lys
          180            185            190
Val Ser Lys Val Val Lys Lys Gly Val Glu Cys Leu Gln Ile Glu Gly
          195            200            205
Thr Leu Lys Lys Ser Leu Asp Phe Lys Asn Asp Ile Asn Ala Glu Ala
          210            215            220
His Ser Trp Gly Met Lys Asn Tyr Glu Glu Trp Ala Lys Asp Leu Thr
          225            230            235            240

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Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg Gln Asp Tyr Lys
 245 250 255
 Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser Gly Asn Glu Lys
 260 265 270
 Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala Leu Gly Lys Lys Pro
 275 280 285
 Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly Met Pro Glu Phe
 290 295 300
 Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys Asp Phe Glu Glu
 305 310 315 320
 Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr Met Ser Thr Ser
 325 330 335
 Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg Lys Ile Ile Leu
 340 345 350
 Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr Leu Ser Ala Ile
 355 360 365
 Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp Lys Asp Ser Lys
 370 375 380
 Tyr His Ile Asp Lys Val Thr Glu Val Ile Ile Lys Gly Val Lys Arg
 385 390 395 400
 Tyr Val Val Asp Ala Thr Leu Leu Thr Asn
 405 410

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide encoding vacuolar targetting peptide used to construct pCIB5533"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCGCGGGCGT GCACTGCCTC AGCAGCAGCA GCTTCGCCGA CAGCAACCCC ATCCGCGTGA

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CCGACCGCGC CGCCAGCACC CTGCAG

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(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 9..1355
- (D) OTHER INFORMATION: /note= "Maize optimized VIP2A(a) with the Bacillus secretion signal removed and the vacuolar targetting signal inserted as contained in pCIB5533"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATCCACC ATG GGC TGG AGC TGG ATC TTC CTG TTC CTG CTG AGC GGC GCC	50
Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala	
415 420	
GCG GGC GTG CAC TGC CTC AGC AGC AGC AGC TTC GCC GAC AGC AAC CCC	98
Ala Gly Val His Cys Leu Ser Ser Ser Ser Phe Ala Asp Ser Asn Pro	
425 430 435 440	
ATC CGC GTG ACC GAC CGC GCC GCC AGC ACC CTG CAG AAC CTG AAG ATC	146
Ile Arg Val Thr Asp Arg Ala Ala Ser Thr Leu Gln Asn Leu Lys Ile	
445 450 455	
ACC GAC AAG GTG GAG GAC TTC AAG GAG GAC AAG GAG AAG GCC AAG GAG	194
Thr Asp Lys Val Glu Asp Phe Lys Glu Asp Lys Glu Lys Ala Lys Glu	
460 465 470	
TGG GGC AAG GAG AAG GAG AAG GAG TGG AAG CTT ACC GCC ACC GAG AAG	242
Trp Gly Lys Glu Lys Glu Lys Glu Trp Lys Leu Thr Ala Thr Glu Lys	
475 480 485	
GGC AAG ATG AAC AAC TTC CTG GAC AAC AAG AAC GAC ATC AAG ACC AAC	290
Gly Lys Met Asn Asn Phe Leu Asp Asn Lys Asn Asp Ile Lys Thr Asn	
490 495 500	
TAC AAG GAG ATC ACC TTC AGC ATA GCC GGC AGC TTC GAG GAC GAG ATC	338
Tyr Lys Glu Ile Thr Phe Ser Ile Ala Gly Ser Phe Glu Asp Glu Ile	
505 510 515 520	
AAG GAC CTG AAG GAG ATC GAC AAG ATG TTC GAC AAG ACC AAC CTG AGC	386

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Lys	Asp	Leu	Lys	Glu	Ile	Asp	Lys	Met	Phe	Asp	Lys	Thr	Asn	Leu	Ser	
				525					530					535		
AAC	AGC	ATC	ATC	ACC	TAC	AAG	AAC	GTG	GAG	CCC	ACC	ACC	ATC	GGC	TTC	434
Asn	Ser	Ile	Ile	Thr	Tyr	Lys	Asn	Val	Glu	Pro	Thr	Thr	Ile	Gly	Phe	
			540					545					550			
AAC	AAG	AGC	CTG	ACC	GAG	GGC	AAC	ACC	ATC	AAC	AGC	GAC	GCC	ATG	GCC	482
Asn	Lys	Ser	Leu	Thr	Glu	Gly	Asn	Thr	Ile	Asn	Ser	Asp	Ala	Met	Ala	
		555					560					565				
CAG	TTC	AAG	GAG	CAG	TTC	CTG	GAC	CGC	GAC	ATC	AAG	TTC	GAC	AGC	TAC	530
Gln	Phe	Lys	Glu	Gln	Phe	Leu	Asp	Arg	Asp	Ile	Lys	Phe	Asp	Ser	Tyr	
	570					575					580					
CTG	GAC	ACC	CAC	CTG	ACC	GCC	CAG	CAG	GTG	AGC	AGC	AAG	GAG	CGC	GTG	578
Leu	Asp	Thr	His	Leu	Thr	Ala	Gln	Gln	Val	Ser	Ser	Lys	Glu	Arg	Val	
585					590					595				600		
ATC	CTG	AAG	GTG	ACC	GTC	CCC	AGC	GGC	AAG	GGC	AGC	ACC	ACC	CCC	ACC	626
Ile	Leu	Lys	Val	Thr	Val	Pro	Ser	Gly	Lys	Gly	Ser	Thr	Thr	Pro	Thr	
			605						610					615		
AAG	GCC	GGC	GTG	ATC	CTG	AAC	AAC	AGC	GAG	TAC	AAG	ATG	CTG	ATC	GAC	674
Lys	Ala	Gly	Val	Ile	Leu	Asn	Asn	Ser	Glu	Tyr	Lys	Met	Leu	Ile	Asp	
			620					625					630			
AAC	GGC	TAC	ATG	GTG	CAC	GTG	GAC	AAG	GTG	AGC	AAG	GTG	GTG	AAG	AAG	722
Asn	Gly	Tyr	Met	Val	His	Val	Asp	Lys	Val	Ser	Lys	Val	Val	Lys	Lys	
		635					640					645				
GGC	GTG	GAG	TGC	CTC	CAG	ATC	GAG	GGC	ACC	CTG	AAG	AAG	AGT	CTA	GAC	770
Gly	Val	Glu	Cys	Leu	Gln	Ile	Glu	Gly	Thr	Leu	Lys	Lys	Ser	Leu	Asp	
	650					655					660					
TTC	AAG	AAC	GAC	ATC	AAC	GCC	GAG	GCC	CAC	AGC	TGG	GGC	ATG	AAG	AAC	818
Phe	Lys	Asn	Asp	Ile	Asn	Ala	Glu	Ala	His	Ser	Trp	Gly	Met	Lys	Asn	
665					670					675				680		
TAC	GAG	GAG	TGG	GCC	AAG	GAC	CTG	ACC	GAC	AGC	CAG	CGC	GAG	GCC	CTG	866
Tyr	Glu	Glu	Trp	Ala	Lys	Asp	Leu	Thr	Asp	Ser	Gln	Arg	Glu	Ala	Leu	
			685						690					695		
GAC	GGC	TAC	GCC	CGC	CAG	GAC	TAC	AAG	GAG	ATC	AAC	AAC	TAC	CTG	CGC	914
Asp	Gly	Tyr	Ala	Arg	Gln	Asp	Tyr	Lys	Glu	Ile	Asn	Asn	Tyr	Leu	Arg	
			700					705					710			
AAC	CAG	GGC	GGC	AGC	GGC	AAC	GAG	AAG	CTG	GAC	GCC	CAG	ATC	AAG	AAC	962
Asn	Gln	Gly	Gly	Ser	Gly	Asn	Glu	Lys	Leu	Asp	Ala	Gln	Ile	Lys	Asn	
		715					720					725				
ATC	AGC	GAC	GCC	CTG	GGC	AAG	AAG	CCC	ATC	CCC	GAG	AAC	ATC	ACC	GTG	1010
Ile	Ser	Asp	Ala	Leu	Gly	Lys	Lys	Pro	Ile	Pro	Glu	Asn	Ile	Thr	Val	
		730				735					740					

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TAC CGC TGG TGC GGC ATG CCC GAG TTC GGC TAC CAG ATC AGC GAC CCC Tyr Arg Trp Cys Gly Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro 745 750 755 760	1058
CTG CCC AGC CTG AAG GAC TTC GAG GAG CAG TTC CTG AAC ACC ATC AAG Leu Pro Ser Leu Lys Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys 765 770 775	1106
GAG GAC AAG GGC TAC ATG AGC ACC AGC CTG AGC AGC GAG CGC CTG GCC Glu Asp Lys Gly Tyr Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala 780 785 790	1154
GCC TTC GGC AGC CGC AAG ATC ATC CTG CGC CTG CAG GTG CCC AAG GGC Ala Phe Gly Ser Arg Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly 795 800 805	1202
AGC ACT GGT GCC TAC CTG AGC GCC ATC GGC GGC TTC GCC AGC GAG AAG Ser Thr Gly Ala Tyr Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys 810 815 820	1250
GAG ATC CTG CTG GAT AAG GAC AGC AAG TAC CAC ATC GAC AAG GTG ACC Glu Ile Leu Leu Asp Lys Asp Ser Lys Tyr His Ile Asp Lys Val Thr 825 830 835 840	1298
GAG GTG ATC ATC AAG GGC GTG AAG CGC TAC GTG GTG GAC GCC ACC CTG Glu Val Ile Ile Lys Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu 845 850 855	1346
CTG ACC AAC TAG Leu Thr Asn	1358

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly 1 5 10 15
Val His Cys Leu Ser Ser Ser Ser Phe Ala Asp Ser Asn Pro Ile Arg 20 25 30
Val Thr Asp Arg Ala Ala Ser Thr Leu Gln Asn Leu Lys Ile Thr Asp 35 40 45
Lys Val Glu Asp Phe Lys Glu Asp Lys Glu Lys Ala Lys Glu Trp Gly 50 55 60

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Lys Glu Lys Glu Lys Glu Trp Lys Leu Thr Ala Thr Glu Lys Gly Lys
 65 70 75 80
 Met Asn Asn Phe Leu Asp Asn Lys Asn Asp Ile Lys Thr Asn Tyr Lys
 85 90 95
 Glu Ile Thr Phe Ser Ile Ala Gly Ser Phe Glu Asp Glu Ile Lys Asp
 100 105 110
 Leu Lys Glu Ile Asp Lys Met Phe Asp Lys Thr Asn Leu Ser Asn Ser
 115 120 125
 Ile Ile Thr Tyr Lys Asn Val Glu Pro Thr Thr Ile Gly Phe Asn Lys
 130 135 140
 Ser Leu Thr Glu Gly Asn Thr Ile Asn Ser Asp Ala Met Ala Gln Phe
 145 150 155 160
 Lys Glu Gln Phe Leu Asp Arg Asp Ile Lys Phe Asp Ser Tyr Leu Asp
 165 170 175
 Thr His Leu Thr Ala Gln Gln Val Ser Ser Lys Glu Arg Val Ile Leu
 180 185 190
 Lys Val Thr Val Pro Ser Gly Lys Gly Ser Thr Thr Pro Thr Lys Ala
 195 200 205
 Gly Val Ile Leu Asn Asn Ser Glu Tyr Lys Met Leu Ile Asp Asn Gly
 210 215 220
 Tyr Met Val His Val Asp Lys Val Ser Lys Val Val Lys Lys Gly Val
 225 230 235 240
 Glu Cys Leu Gln Ile Glu Gly Thr Leu Lys Lys Ser Leu Asp Phe Lys
 245 250 255
 Asn Asp Ile Asn Ala Glu Ala His Ser Trp Gly Met Lys Asn Tyr Glu
 260 265 270
 Glu Trp Ala Lys Asp Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly
 275 280 285
 Tyr Ala Arg Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln
 290 295 300
 Gly Gly Ser Gly Asn Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser
 305 310 315 320
 Asp Ala Leu Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg
 325 330 335
 Trp Cys Gly Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro
 340 345 350

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Ser Leu Lys Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp
 355 360 365

Lys Gly Tyr Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe
 370 375 380

Gly Ser Arg Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr
 385 390 395 400

Gly Ala Tyr Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile
 405 410 415

Leu Leu Asp Lys Asp Ser Lys Tyr His Ile Asp Lys Val Thr Glu Val
 420 425 430

Ile Ile Lys Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr
 435 440 445

Asn

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "linker peptide for fusion of VIP1A(a) and VIP2A(a) used to construct pCIB5533"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

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(A) DESCRIPTION: /desc = "DNA encoding linker peptide used to construct pCIB5533"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```
CCCGGGCCTT CTACTCCCC AACTCCCTCT CCTAGCACGC CTCCGACACC TAGCGATATC 60
GGATCC 66
```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4031 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 6..4019
- (D) OTHER INFORMATION: /note= "Maize optimized DNA sequence encoding a VIP2A(a) - VIP1A(a) fusion protein as contained in pCIB5531"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```
GATCC ATG AAG CGC ATG GAG GGC AAG CTG TTC ATG GTG AGC AAG AAG 47
      Met Lys Arg Met Glu Gly Lys Leu Phe Met Val Ser Lys Lys
      450          455          460

CTC CAG GTG GTG ACC AAG ACC GTG CTG CTG AGC ACC GTG TTC AGC ATC 95
Leu Gln Val Val Thr Lys Thr Val Leu Leu Ser Thr Val Phe Ser Ile
465          470          475

AGC CTG CTG AAC AAC GAG GTG ATC AAG GCC GAG CAG CTG AAC ATC AAC 143
Ser Leu Leu Asn Asn Glu Val Ile Lys Ala Glu Gln Leu Asn Ile Asn
480          485          490          495

AGC CAG AGC AAG TAC ACC AAC CTC CAG AAC CTG AAG ATC ACC GAC AAG 191
Ser Gln Ser Lys Tyr Thr Asn Leu Gln Asn Leu Lys Ile Thr Asp Lys
      500          505          510

GTG GAG GAC TTC AAG GAG GAC AAG GAG AAG GCC AAG GAG TGG GGC AAG 239
```

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Val	Glu	Asp	Phe	Lys	Glu	Asp	Lys	Glu	Lys	Ala	Lys	Glu	Trp	Gly	Lys	
			515					520					525			
GAG	AAG	GAG	AAG	GAG	TGG	AAG	CTT	ACC	GCC	ACC	GAG	AAG	GGC	AAG	ATG	287
Glu	Lys	Glu	Lys	Glu	Trp	Lys	Leu	Thr	Ala	Thr	Glu	Lys	Gly	Lys	Met	
			530				535						540			
AAC	AAC	TTC	CTG	GAC	AAC	AAG	AAC	GAC	ATC	AAG	ACC	AAC	TAC	AAG	GAG	335
Asn	Asn	Phe	Leu	Asp	Asn	Lys	Asn	Asp	Ile	Lys	Thr	Asn	Tyr	Lys	Glu	
			545				550					555				
ATC	ACC	TTC	AGC	ATA	GCC	GGC	AGC	TTC	GAG	GAC	GAG	ATC	AAG	GAC	CTG	383
Ile	Thr	Phe	Ser	Ile	Ala	Gly	Ser	Phe	Glu	Asp	Glu	Ile	Lys	Asp	Leu	
					565					570					575	
AAG	GAG	ATC	GAC	AAG	ATG	TTC	GAC	AAG	ACC	AAC	CTG	AGC	AAC	AGC	ATC	431
Lys	Glu	Ile	Asp	Lys	Met	Phe	Asp	Lys	Thr	Asn	Leu	Ser	Asn	Ser	Ile	
				580					585					590		
ATC	ACC	TAC	AAG	AAC	GTG	GAG	CCC	ACC	ACC	ATC	GGC	TTC	AAC	AAG	AGC	479
Ile	Thr	Tyr	Lys	Asn	Val	Glu	Pro	Thr	Thr	Ile	Gly	Phe	Asn	Lys	Ser	
			595					600					605			
CTG	ACC	GAG	GGC	AAC	ACC	ATC	AAC	AGC	GAC	GCC	ATG	GCC	CAG	TTC	AAG	527
Leu	Thr	Glu	Gly	Asn	Thr	Ile	Asn	Ser	Asp	Ala	Met	Ala	Gln	Phe	Lys	
			610				615					620				
GAG	CAG	TTC	CTG	GAC	CGC	GAC	ATC	AAG	TTC	GAC	AGC	TAC	CTG	GAC	ACC	575
Glu	Gln	Phe	Leu	Asp	Arg	Asp	Ile	Lys	Phe	Asp	Ser	Tyr	Leu	Asp	Thr	
			625				630					635				
CAC	CTG	ACC	GCC	CAG	CAG	GTG	AGC	AGC	AAG	GAG	CGC	GTG	ATC	CTG	AAG	623
His	Leu	Thr	Ala	Gln	Gln	Val	Ser	Ser	Lys	Glu	Arg	Val	Ile	Leu	Lys	
					645					650					655	
GTG	ACC	GTC	CCC	AGC	GGC	AAG	GGC	AGC	ACC	ACC	CCC	ACC	AAG	GCC	GGC	671
Val	Thr	Val	Pro	Ser	Gly	Lys	Gly	Ser	Thr	Thr	Pro	Thr	Lys	Ala	Gly	
				660					665					670		
GTG	ATC	CTG	AAC	AAC	AGC	GAG	TAC	AAG	ATG	CTG	ATC	GAC	AAC	GGC	TAC	719
Val	Ile	Leu	Asn	Asn	Ser	Glu	Tyr	Lys	Met	Leu	Ile	Asp	Asn	Gly	Tyr	
			675					680					685			
ATG	GTG	CAC	GTG	GAC	AAG	GTG	AGC	AAG	GTG	GTG	AAG	AAG	GGC	GTG	GAG	767
Met	Val	His	Val	Asp	Lys	Val	Ser	Lys	Val	Val	Lys	Lys	Gly	Val	Glu	
			690					695				700				
TGC	CTC	CAG	ATC	GAG	GGC	ACC	CTG	AAG	AAG	AGT	CTA	GAC	TTC	AAG	AAC	815
Cys	Leu	Gln	Ile	Glu	Gly	Thr	Leu	Lys	Lys	Ser	Leu	Asp	Phe	Lys	Asn	
			705				710					715				
GAC	ATC	AAC	GCC	GAG	GCC	CAC	AGC	TGG	GGC	ATG	AAG	AAC	TAC	GAG	GAG	863
Asp	Ile	Asn	Ala	Glu	Ala	His	Ser	Trp	Gly	Met	Lys	Asn	Tyr	Glu	Glu	
					725					730					735	

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TGG GCC AAG GAC CTG ACC GAC AGC CAG CGC GAG GCC CTG GAC GGC TAC	911
Trp Ala Lys Asp Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr	
740 745 750	
GCC CGC CAG GAC TAC AAG GAG ATC AAC AAC TAC CTG CGC AAC CAG GGC	959
Ala Arg Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly	
755 760 765	
GGC AGC GGC AAC GAG AAG CTG GAC GCC CAG ATC AAG AAC ATC AGC GAC	1007
Gly Ser Gly Asn Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp	
770 775 780	
GCC CTG GGC AAG AAG CCC ATC CCC GAG AAC ATC ACC GTG TAC CGC TGG	1055
Ala Leu Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp	
785 790 795	
TGC GGC ATG CCC GAG TTC GGC TAC CAG ATC AGC GAC CCC CTG CCC AGC	1103
Cys Gly Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser	
800 805 810 815	
CTG AAG GAC TTC GAG GAG CAG TTC CTG AAC ACC ATC AAG GAG GAC AAG	1151
Leu Lys Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys	
820 825 830	
GGC TAC ATG AGC ACC AGC CTG AGC AGC GAG CGC CTG GCC GCC TTC GGC	1199
Gly Tyr Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly	
835 840 845	
AGC CGC AAG ATC ATC CTG CGC CTG CAG GTG CCC AAG GGC AGC ACT GGT	1247
Ser Arg Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly	
850 855 860	
GCC TAC CTG AGC GCC ATC GGC GGC TTC GCC AGC GAG AAG GAG ATC CTG	1295
Ala Tyr Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu	
865 870 875	
CTG GAT AAG GAC AGC AAG TAC CAC ATC GAC AAG GTG ACC GAG GTG ATC	1343
Leu Asp Lys Asp Ser Lys Tyr His Ile Asp Lys Val Thr Glu Val Ile	
880 885 890 895	
ATC AAG GGC GTG AAG CGC TAC GTG GTG GAC GCC ACC CTG CTG ACC AAC	1391
Ile Lys Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn	
900 905 910	
TCC CGG GGG CCT TCT ACT CCC CCA ACT CCC TCT CCT AGC ACG CCT CCG	1439
Ser Arg Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro	
915 920 925	
ACA CCT AGC GAT ATC GGA TCC ACC ATG AAG ACC AAC CAG ATC AGC ACC	1487
Thr Pro Ser Asp Ile Gly Ser Thr Met Lys Thr Asn Gln Ile Ser Thr	
930 935 940	
ACC CAG AAG AAC CAG CAG AAG GAG ATG GAC CGC AAG GGC CTG CTG GGC	1535
Thr Gln Lys Asn Gln Gln Lys Glu Met Asp Arg Lys Gly Leu Leu Gly	
945 950 955	

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TAC	TAC	TTC	AAG	GGC	AAG	GAC	TTC	AGC	AAC	CTG	ACC	ATG	TTC	GCC	CCC	1583
Tyr	Tyr	Phe	Lys	Gly	Lys	Asp	Phe	Ser	Asn	Leu	Thr	Met	Phe	Ala	Pro	
960					965					970					975	
ACG	CGT	GAC	AGC	ACC	CTG	ATC	TAC	GAC	CAG	CAG	ACC	GCC	AAC	AAG	CTG	1631
Thr	Arg	Asp	Ser	Thr	Leu	Ile	Tyr	Asp	Gln	Gln	Thr	Ala	Asn	Lys	Leu	
				980					985					990		
CTG	GAC	AAG	AAG	CAG	CAG	GAG	TAC	CAG	AGC	ATC	CGC	TGG	ATC	GGC	CTG	1679
Leu	Asp	Lys	Lys	Gln	Gln	Glu	Tyr	Gln	Ser	Ile	Arg	Trp	Ile	Gly	Leu	
			995					1000					1005			
ATC	CAG	AGC	AAG	GAG	ACC	GGC	GAC	TTC	ACC	TTC	AAC	CTG	AGC	GAG	GAC	1727
Ile	Gln	Ser	Lys	Glu	Thr	Gly	Asp	Phe	Thr	Phe	Asn	Leu	Ser	Glu	Asp	
		1010					1015					1020				
GAG	CAG	GCC	ATC	ATC	GAG	ATC	AAC	GGC	AAG	ATC	ATC	AGC	AAC	AAG	GGC	1775
Glu	Gln	Ala	Ile	Ile	Glu	Ile	Asn	Gly	Lys	Ile	Ile	Ser	Asn	Lys	Gly	
	1025					1030					1035					
AAG	GAG	AAG	CAG	GTG	GTG	CAC	CTG	GAG	AAG	GGC	AAG	CTG	GTG	CCC	ATC	1823
Lys	Glu	Lys	Gln	Val	Val	His	Leu	Glu	Lys	Gly	Lys	Leu	Val	Pro	Ile	
1040					1045					1050					1055	
AAG	ATC	GAG	TAC	CAG	AGC	GAC	ACC	AAG	TTC	AAC	ATC	GAC	AGC	AAG	ACC	1871
Lys	Ile	Glu	Tyr	Gln	Ser	Asp	Thr	Lys	Phe	Asn	Ile	Asp	Ser	Lys	Thr	
				1060					1065					1070		
TTC	AAG	GAG	CTG	AAG	CTT	TTC	AAG	ATC	GAC	AGC	CAG	AAC	CAG	CCC	CAG	1919
Phe	Lys	Glu	Leu	Lys	Leu	Phe	Lys	Ile	Asp	Ser	Gln	Asn	Gln	Pro	Gln	
			1075					1080					1085			
CAG	GTG	CAG	CAG	GAC	GAG	CTG	CGC	AAC	CCC	GAG	TTC	AAC	AAG	AAG	GAG	1967
Gln	Val	Gln	Gln	Asp	Glu	Leu	Arg	Asn	Pro	Glu	Phe	Asn	Lys	Lys	Glu	
		1090					1095					1100				
AGC	CAG	GAG	TTC	CTG	GCC	AAG	CCC	AGC	AAG	ATC	AAC	CTG	TTC	ACC	CAG	2015
Ser	Gln	Glu	Phe	Leu	Ala	Lys	Pro	Ser	Lys	Ile	Asn	Leu	Phe	Thr	Gln	
	1105					1110					1115					
CAG	ATG	AAG	CGC	GAG	ATC	GAC	GAG	GAC	ACC	GAC	ACC	GAC	GGC	GAC	AGC	2063
Gln	Met	Lys	Arg	Glu	Ile	Asp	Glu	Asp	Thr	Asp	Thr	Asp	Gly	Asp	Ser	
1120					1125					1130					1135	
ATC	CCC	GAC	CTG	TGG	GAG	GAG	AAC	GGC	TAC	ACC	ATC	CAG	AAC	CGC	ATC	2111
Ile	Pro	Asp	Leu	Trp	Glu	Glu	Asn	Gly	Tyr	Thr	Ile	Gln	Asn	Arg	Ile	
				1140					1145					1150		
GCC	GTG	AAG	TGG	GAC	GAC	AGC	CTG	GCT	AGC	AAG	GGC	TAC	ACC	AAG	TTC	2159
Ala	Val	Lys	Trp	Asp	Asp	Ser	Leu	Ala	Ser	Lys	Gly	Tyr	Thr	Lys	Phe	
			1155					1160					1165			
GTG	AGC	AAC	CCC	CTG	GAG	AGC	CAC	ACC	GTG	GGC	GAC	CCC	TAC	ACC	GAC	2207
Val	Ser	Asn	Pro	Leu	Glu	Ser	His	Thr	Val	Gly	Asp	Pro	Tyr	Thr	Asp	

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1170	1175	1180	
TAC GAG AAG GCC GCC CGC GAC CTG GAC CTG AGC AAC GCC AAG GAG ACC Tyr Glu Lys Ala Ala Arg Asp Leu Asp Leu Ser Asn Ala Lys Glu Thr 1185 1190 1195			2255
TTC AAC CCC CTG GTG GCC GCC TTC CCC AGC GTG AAC GTG AGC ATG GAG Phe Asn Pro Leu Val Ala Ala Phe Pro Ser Val Asn Val Ser Met Glu 1200 1205 1210 1215			2303
AAG GTG ATC CTG AGC CCC AAC GAG AAC CTG AGC AAC AGC GTG GAG AGC Lys Val Ile Leu Ser Pro Asn Glu Asn Leu Ser Asn Ser Val Glu Ser 1220 1225 1230			2351
CAC TCG AGC ACC AAC TGG AGC TAC ACC AAC ACC GAG GGC GCC AGC GTG His Ser Ser Thr Asn Trp Ser Tyr Thr Asn Thr Glu Gly Ala Ser Val 1235 1240 1245			2399
GAG GCC GGC ATC GGT CCC AAG GGC ATC AGC TTC GGC GTG AGC GTG AAC Glu Ala Gly Ile Gly Pro Lys Gly Ile Ser Phe Gly Val Ser Val Asn 1250 1255 1260			2447
TAC CAG CAC AGC GAG ACC GTG GCC CAG GAG TGG GGC ACC AGC ACC GGC Tyr Gln His Ser Glu Thr Val Ala Gln Glu Trp Gly Thr Ser Thr Gly 1265 1270 1275			2495
AAC ACC AGC CAG TTC AAC ACC GCC AGC GCC GGC TAC CTG AAC GCC AAC Asn Thr Ser Gln Phe Asn Thr Ala Ser Ala Gly Tyr Leu Asn Ala Asn 1280 1285 1290 1295			2543
GTG CGC TAC AAC AAC GTG GGC ACC GGC GCC ATC TAC GAC GTG AAG CCC Val Arg Tyr Asn Asn Val Gly Thr Gly Ala Ile Tyr Asp Val Lys Pro 1300 1305 1310			2591
ACC ACC AGC TTC GTG CTG AAC AAC GAC ACC ATC GCC ACC ATC ACC GCC Thr Thr Ser Phe Val Leu Asn Asn Asp Thr Ile Ala Thr Ile Thr Ala 1315 1320 1325			2639
AAG TCG AAT TCC ACC GCC CTG AAC ATC AGC CCC GGC GAG AGC TAC CCC Lys Ser Asn Ser Thr Ala Leu Asn Ile Ser Pro Gly Glu Ser Tyr Pro 1330 1335 1340			2687
AAG AAG GGC CAG AAC GGC ATC GCC ATC ACC AGC ATG GAC GAC TTC AAC Lys Lys Gly Gln Asn Gly Ile Ala Ile Thr Ser Met Asp Asp Phe Asn 1345 1350 1355			2735
AGC CAC CCC ATC ACC CTG AAC AAG AAG CAG GTG GAC AAC CTG CTG AAC Ser His Pro Ile Thr Leu Asn Lys Lys Gln Val Asp Asn Leu Leu Asn 1360 1365 1370 1375			2783
AAC AAG CCC ATG ATG CTG GAG ACC AAC CAG ACC GAC GGC GTC TAC AAG Asn Lys Pro Met Met Leu Glu Thr Asn Gln Thr Asp Gly Val Tyr Lys 1380 1385 1390			2831
ATC AAG GAC ACC CAC GGC AAC ATC GTG ACG GGC GGC GAG TGG AAC GGC			2879

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Ile Lys Asp Thr His Gly Asn Ile Val Thr Gly Gly Glu Trp Asn Gly	
1395 1400 1405	
GTG ATC CAG CAG ATC AAG GCC AAG ACC GCC AGC ATC ATC GTC GAC GAC	2927
Val Ile Gln Gln Ile Lys Ala Lys Thr Ala Ser Ile Ile Val Asp Asp	
1410 1415 1420	
GGC GAG CGC GTG GCC GAG AAG CGC GTG GCC GCC AAG GAC TAC GAG AAC	2975
Gly Glu Arg Val Ala Glu Lys Arg Val Ala Ala Lys Asp Tyr Glu Asn	
1425 1430 1435	
CCC GAG GAC AAG ACC CCC AGC CTG ACC CTG AAG GAC GCC CTG AAG CTG	3023
Pro Glu Asp Lys Thr Pro Ser Leu Thr Leu Lys Asp Ala Leu Lys Leu	
1440 1445 1450 1455	
AGC TAC CCC GAC GAG ATC AAG GAG ATC GAG GGC TTG CTG TAC TAC AAG	3071
Ser Tyr Pro Asp Glu Ile Lys Glu Ile Glu Gly Leu Leu Tyr Tyr Lys	
1460 1465 1470	
AAC AAG CCC ATC TAC GAG AGC AGC GTG ATG ACC TAT CTA GAC GAG AAC	3119
Asn Lys Pro Ile Tyr Glu Ser Ser Val Met Thr Tyr Leu Asp Glu Asn	
1475 1480 1485	
ACC GCC AAG GAG GTG ACC AAG CAG CTG AAC GAC ACC ACC GGC AAG TTC	3167
Thr Ala Lys Glu Val Thr Lys Gln Leu Asn Asp Thr Thr Gly Lys Phe	
1490 1495 1500	
AAG GAC GTG AGC CAC CTG TAC GAC GTG AAG CTG ACC CCC AAG ATG AAC	3215
Lys Asp Val Ser His Leu Tyr Asp Val Lys Leu Thr Pro Lys Met Asn	
1505 1510 1515	
GTG ACC ATC AAG CTG AGC ATC CTG TAC GAC AAC GCC GAG AGC AAC GAC	3263
Val Thr Ile Lys Leu Ser Ile Leu Tyr Asp Asn Ala Glu Ser Asn Asp	
1520 1525 1530 1535	
AAC AGC ATC GGC AAG TGG ACC AAC ACC AAC ATC GTG AGC GGC GGC AAC	3311
Asn Ser Ile Gly Lys Trp Thr Asn Thr Asn Ile Val Ser Gly Gly Asn	
1540 1545 1550	
AAC GGC AAG AAG CAG TAC AGC AGC AAC AAC CCC GAC GCC AAC CTG ACC	3359
Asn Gly Lys Lys Gln Tyr Ser Ser Asn Asn Pro Asp Ala Asn Leu Thr	
1555 1560 1565	
CTG AAC ACC GAC GCC CAG GAG AAG CTG AAC AAG AAC CGC GAC TAC TAC	3407
Leu Asn Thr Asp Ala Gln Glu Lys Leu Asn Lys Asn Arg Asp Tyr Tyr	
1570 1575 1580	
ATC AGC CTG TAC ATG AAG AGC GAG AAG AAC ACC CAG TGC GAG ATC ACC	3455
Ile Ser Leu Tyr Met Lys Ser Glu Lys Asn Thr Gln Cys Glu Ile Thr	
1585 1590 1595	
ATC GAC GGC GAG ATA TAC CCC ATC ACC ACC AAG ACC GTG AAC GTG AAC	3503
Ile Asp Gly Glu Ile Tyr Pro Ile Thr Thr Lys Thr Val Asn Val Asn	
1600 1605 1610 1615	

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AAG GAC AAC TAC AAG CGC CTG GAC ATC ATC GCC CAC AAC ATC AAG AGC Lys Asp Asn Tyr Lys Arg Leu Asp Ile Ile Ala His Asn Ile Lys Ser 1620 1625 1630	3551
AAC CCC ATC AGC AGC CTG CAC ATC AAG ACC AAC GAC GAG ATC ACC CTG Asn Pro Ile Ser Ser Leu His Ile Lys Thr Asn Asp Glu Ile Thr Leu 1635 1640 1645	3599
TTC TGG GAC GAC ATA TCG ATT ACC GAC GTC GCC AGC ATC AAG CCC GAG Phe Trp Asp Asp Ile Ser Ile Thr Asp Val Ala Ser Ile Lys Pro Glu 1650 1655 1660	3647
AAC CTG ACC GAC AGC GAG ATC AAG CAG ATA TAC AGT CGC TAC GGC ATC Asn Leu Thr Asp Ser Glu Ile Lys Gln Ile Tyr Ser Arg Tyr Gly Ile 1665 1670 1675	3695
AAG CTG GAG GAC GGC ATC CTG ATC GAC AAG AAA GGC GGC ATC CAC TAC Lys Leu Glu Asp Gly Ile Leu Ile Asp Lys Lys Gly Gly Ile His Tyr 1680 1685 1690 1695	3743
GGC GAG TTC ATC AAC GAG GCC AGC TTC AAC ATC GAG CCC CTG CAG AAC Gly Glu Phe Ile Asn Glu Ala Ser Phe Asn Ile Glu Pro Leu Gln Asn 1700 1705 1710	3791
TAC GTG ACC AAG TAC GAG GTG ACC TAC AGC AGC GAG CTG GGC CCC AAC Tyr Val Thr Lys Tyr Glu Val Thr Tyr Ser Ser Glu Leu Gly Pro Asn 1715 1720 1725	3839
GTG AGC GAC ACC CTG GAG AGC GAC AAG ATT TAC AAG GAC GGC ACC ATC Val Ser Asp Thr Leu Glu Ser Asp Lys Ile Tyr Lys Asp Gly Thr Ile 1730 1735 1740	3887
AAG TTC GAC TTC ACC AAG TAC AGC AAG AAC GAG CAG GGC CTG TTC TAC Lys Phe Asp Phe Thr Lys Tyr Ser Lys Asn Glu Gln Gly Leu Phe Tyr 1745 1750 1755	3935
GAC AGC GGC CTG AAC TGG GAC TTC AAG ATC AAC GCC ATC ACC TAC GAC Asp Ser Gly Leu Asn Trp Asp Phe Lys Ile Asn Ala Ile Thr Tyr Asp 1760 1765 1770 1775	3983
GGC AAG GAG ATG AAC GTG TTC CAC CGC TAC AAC AAG TAGATCTGAG Gly Lys Glu Met Asn Val Phe His Arg Tyr Asn Lys 1780 1785	4029
CT	4031

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met	Lys	Arg	Met	Glu	Gly	Lys	Leu	Phe	Met	Val	Ser	Lys	Lys	Leu	Gln	1	5	10	15
Val	Val	Thr	Lys	Thr	Val	Leu	Leu	Ser	Thr	Val	Phe	Ser	Ile	Ser	Leu	20	25	30	
Leu	Asn	Asn	Glu	Val	Ile	Lys	Ala	Glu	Gln	Leu	Asn	Ile	Asn	Ser	Gln	35	40	45	
Ser	Lys	Tyr	Thr	Asn	Leu	Gln	Asn	Leu	Lys	Ile	Thr	Asp	Lys	Val	Glu	50	55	60	
Asp	Phe	Lys	Glu	Asp	Lys	Glu	Lys	Ala	Lys	Glu	Trp	Gly	Lys	Glu	Lys	65	70	75	80
Glu	Lys	Glu	Trp	Lys	Leu	Thr	Ala	Thr	Glu	Lys	Gly	Lys	Met	Asn	Asn	85	90	95	
Phe	Leu	Asp	Asn	Lys	Asn	Asp	Ile	Lys	Thr	Asn	Tyr	Lys	Glu	Ile	Thr	100	105	110	
Phe	Ser	Ile	Ala	Gly	Ser	Phe	Glu	Asp	Glu	Ile	Lys	Asp	Leu	Lys	Glu	115	120	125	
Ile	Asp	Lys	Met	Phe	Asp	Lys	Thr	Asn	Leu	Ser	Asn	Ser	Ile	Ile	Thr	130	135	140	
Tyr	Lys	Asn	Val	Glu	Pro	Thr	Thr	Ile	Gly	Phe	Asn	Lys	Ser	Leu	Thr	145	150	155	160
Glu	Gly	Asn	Thr	Ile	Asn	Ser	Asp	Ala	Met	Ala	Gln	Phe	Lys	Glu	Gln	165	170	175	
Phe	Leu	Asp	Arg	Asp	Ile	Lys	Phe	Asp	Ser	Tyr	Leu	Asp	Thr	His	Leu	180	185	190	
Thr	Ala	Gln	Gln	Val	Ser	Ser	Lys	Glu	Arg	Val	Ile	Leu	Lys	Val	Thr	195	200	205	
Val	Pro	Ser	Gly	Lys	Gly	Ser	Thr	Thr	Pro	Thr	Lys	Ala	Gly	Val	Ile	210	215	220	
Leu	Asn	Asn	Ser	Glu	Tyr	Lys	Met	Leu	Ile	Asp	Asn	Gly	Tyr	Met	Val	225	230	235	240
His	Val	Asp	Lys	Val	Ser	Lys	Val	Val	Lys	Lys	Gly	Val	Glu	Cys	Leu	245	250	255	
Gln	Ile	Glu	Gly	Thr	Leu	Lys	Lys	Ser	Leu	Asp	Phe	Lys	Asn	Asp	Ile	260	265	270	
Asn	Ala	Glu	Ala	His	Ser	Trp	Gly	Met	Lys	Asn	Tyr	Glu	Glu	Trp	Ala				

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275	280	285
Lys Asp Leu Thr Asp Ser Gln Arg Glu Ala Leu Asp Gly Tyr Ala Arg		
290	295	300
Gln Asp Tyr Lys Glu Ile Asn Asn Tyr Leu Arg Asn Gln Gly Gly Ser		
305	310	315
Gly Asn Glu Lys Leu Asp Ala Gln Ile Lys Asn Ile Ser Asp Ala Leu		
	325	330
Gly Lys Lys Pro Ile Pro Glu Asn Ile Thr Val Tyr Arg Trp Cys Gly		
	340	345
Met Pro Glu Phe Gly Tyr Gln Ile Ser Asp Pro Leu Pro Ser Leu Lys		
	355	360
Asp Phe Glu Glu Gln Phe Leu Asn Thr Ile Lys Glu Asp Lys Gly Tyr		
	370	375
Met Ser Thr Ser Leu Ser Ser Glu Arg Leu Ala Ala Phe Gly Ser Arg		
385	390	395
Lys Ile Ile Leu Arg Leu Gln Val Pro Lys Gly Ser Thr Gly Ala Tyr		
	405	410
Leu Ser Ala Ile Gly Gly Phe Ala Ser Glu Lys Glu Ile Leu Leu Asp		
	420	425
Lys Asp Ser Lys Tyr His Ile Asp Lys Val Thr Glu Val Ile Ile Lys		
	435	440
Gly Val Lys Arg Tyr Val Val Asp Ala Thr Leu Leu Thr Asn Ser Arg		
	450	455
Gly Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro		
465	470	475
Ser Asp Ile Gly Ser Thr Met Lys Thr Asn Gln Ile Ser Thr Thr Gln		
	485	490
Lys Asn Gln Gln Lys Glu Met Asp Arg Lys Gly Leu Leu Gly Tyr Tyr		
	500	505
Phe Lys Gly Lys Asp Phe Ser Asn Leu Thr Met Phe Ala Pro Thr Arg		
	515	520
Asp Ser Thr Leu Ile Tyr Asp Gln Gln Thr Ala Asn Lys Leu Leu Asp		
	530	535
Lys Lys Gln Gln Glu Tyr Gln Ser Ile Arg Trp Ile Gly Leu Ile Gln		
545	550	555
Ser Lys Glu Thr Gly Asp Phe Thr Phe Asn Leu Ser Glu Asp Glu Gln		
	565	570

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Ala Ile Ile Glu Ile Asn Gly Lys Ile Ile Ser Asn Lys Gly Lys Glu
 580 585 590
 Lys Gln Val Val His Leu Glu Lys Gly Lys Leu Val Pro Ile Lys Ile
 595 600 605
 Glu Tyr Gln Ser Asp Thr Lys Phe Asn Ile Asp Ser Lys Thr Phe Lys
 610 615 620
 Glu Leu Lys Leu Phe Lys Ile Asp Ser Gln Asn Gln Pro Gln Gln Val
 625 630 635 640
 Gln Gln Asp Glu Leu Arg Asn Pro Glu Phe Asn Lys Lys Glu Ser Gln
 645 650 655
 Glu Phe Leu Ala Lys Pro Ser Lys Ile Asn Leu Phe Thr Gln Gln Met
 660 665 670
 Lys Arg Glu Ile Asp Glu Asp Thr Asp Thr Asp Gly Asp Ser Ile Pro
 675 680 685
 Asp Leu Trp Glu Glu Asn Gly Tyr Thr Ile Gln Asn Arg Ile Ala Val
 690 695 700
 Lys Trp Asp Asp Ser Leu Ala Ser Lys Gly Tyr Thr Lys Phe Val Ser
 705 710 715 720
 Asn Pro Leu Glu Ser His Thr Val Gly Asp Pro Tyr Thr Asp Tyr Glu
 725 730 735
 Lys Ala Ala Arg Asp Leu Asp Leu Ser Asn Ala Lys Glu Thr Phe Asn
 740 745 750
 Pro Leu Val Ala Ala Phe Pro Ser Val Asn Val Ser Met Glu Lys Val
 755 760 765
 Ile Leu Ser Pro Asn Glu Asn Leu Ser Asn Ser Val Glu Ser His Ser
 770 775 780
 Ser Thr Asn Trp Ser Tyr Thr Asn Thr Glu Gly Ala Ser Val Glu Ala
 785 790 795 800
 Gly Ile Gly Pro Lys Gly Ile Ser Phe Gly Val Ser Val Asn Tyr Gln
 805 810 815
 His Ser Glu Thr Val Ala Gln Glu Trp Gly Thr Ser Thr Gly Asn Thr
 820 825 830
 Ser Gln Phe Asn Thr Ala Ser Ala Gly Tyr Leu Asn Ala Asn Val Arg
 835 840 845
 Tyr Asn Asn Val Gly Thr Gly Ala Ile Tyr Asp Val Lys Pro Thr Thr
 850 855 860

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Ser Phe Val Leu Asn Asn Asp Thr Ile Ala Thr Ile Thr Ala Lys Ser
 865 870 875 880
 Asn Ser Thr Ala Leu Asn Ile Ser Pro Gly Glu Ser Tyr Pro Lys Lys
 885 890 895
 Gly Gln Asn Gly Ile Ala Ile Thr Ser Met Asp Asp Phe Asn Ser His
 900 905 910
 Pro Ile Thr Leu Asn Lys Lys Gln Val Asp Asn Leu Leu Asn Asn Lys
 915 920 925
 Pro Met Met Leu Glu Thr Asn Gln Thr Asp Gly Val Tyr Lys Ile Lys
 930 935 940
 Asp Thr His Gly Asn Ile Val Thr Gly Gly Glu Trp Asn Gly Val Ile
 945 950 955 960
 Gln Gln Ile Lys Ala Lys Thr Ala Ser Ile Ile Val Asp Asp Gly Glu
 965 970 975
 Arg Val Ala Glu Lys Arg Val Ala Ala Lys Asp Tyr Glu Asn Pro Glu
 980 985 990
 Asp Lys Thr Pro Ser Leu Thr Leu Lys Asp Ala Leu Lys Leu Ser Tyr
 995 1000 1005
 Pro Asp Glu Ile Lys Glu Ile Glu Gly Leu Leu Tyr Tyr Lys Asn Lys
 1010 1015 1020
 Pro Ile Tyr Glu Ser Ser Val Met Thr Tyr Leu Asp Glu Asn Thr Ala
 1025 1030 1035 1040
 Lys Glu Val Thr Lys Gln Leu Asn Asp Thr Thr Gly Lys Phe Lys Asp
 1045 1050 1055
 Val Ser His Leu Tyr Asp Val Lys Leu Thr Pro Lys Met Asn Val Thr
 1060 1065 1070
 Ile Lys Leu Ser Ile Leu Tyr Asp Asn Ala Glu Ser Asn Asp Asn Ser
 1075 1080 1085
 Ile Gly Lys Trp Thr Asn Thr Asn Ile Val Ser Gly Gly Asn Asn Gly
 1090 1095 1100
 Lys Lys Gln Tyr Ser Ser Asn Asn Pro Asp Ala Asn Leu Thr Leu Asn
 1105 1110 1115 1120
 Thr Asp Ala Gln Glu Lys Leu Asn Lys Asn Arg Asp Tyr Tyr Ile Ser
 1125 1130 1135
 Leu Tyr Met Lys Ser Glu Lys Asn Thr Gln Cys Glu Ile Thr Ile Asp
 1140 1145 1150
 Gly Glu Ile Tyr Pro Ile Thr Thr Lys Thr Val Asn Val Asn Lys Asp

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1155	1160	1165
Asn Tyr Lys Arg Leu Asp	Ile Ile Ala His Asn	Ile Lys Ser Asn Pro
1170	1175	1180
Ile Ser Ser Leu His Ile	Lys Thr Asn Asp Glu	Ile Thr Leu Phe Trp
1185	1190	1195 1200
Asp Asp Ile Ser Ile Thr	Asp Val Ala Ser Ile	Lys Pro Glu Asn Leu
1205	1210	1215
Thr Asp Ser Glu Ile Lys	Gln Ile Tyr Ser Arg	Tyr Gly Ile Lys Leu
1220	1225	1230
Glu Asp Gly Ile Leu Ile	Asp Lys Lys Gly Gly	Ile His Tyr Gly Glu
1235	1240	1245
Phe Ile Asn Glu Ala Ser	Phe Asn Ile Glu Pro	Leu Gln Asn Tyr Val
1250	1255	1260
Thr Lys Tyr Glu Val Thr	Tyr Ser Ser Glu Leu	Gly Pro Asn Val Ser
1265	1270	1275 1280
Asp Thr Leu Glu Ser Asp	Lys Ile Tyr Lys Asp	Gly Thr Ile Lys Phe
1285	1290	1295
Asp Phe Thr Lys Tyr Ser	Lys Asn Glu Gln Gly	Leu Phe Tyr Asp Ser
1300	1305	1310
Gly Leu Asn Trp Asp Phe	Lys Ile Asn Ala Ile	Thr Tyr Asp Gly Lys
1315	1320	1325
Glu Met Asn Val Phe His	Arg Tyr Asn Lys	
1330	1335	

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 17..2444
- (D) OTHER INFORMATION: /product= "3A(a) synthetic:native fusion"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGATCCACCA ATGAAC ATG AAC AAG AAC AAC ACC AAG CTG AGC ACC CGC	49
Met Asn Lys Asn Asn Thr Lys Leu Ser Thr Arg	
1 5 10	
GCC CTG CCG AGC TTC ATC GAC TAC TTC AAC GGC ATC TAC GGC TTC GCC	97
Ala Leu Pro Ser Phe Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala	
15 20 25	
ACC GGC ATC AAG GAC ATC ATG AAC ATG ATC TTC AAG ACC GAC ACC GGC	145
Thr Gly Ile Lys Asp Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly	
30 35 40	
GGC GAC CTG ACC CTG GAC GAG ATC CTG AAG AAC CAG CAG CTG CTG AAC	193
Gly Asp Leu Thr Leu Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn	
45 50 55	
GAC ATC AGC GGC AAG CTG GAC GGC GTG AAC GGC AGC CTG AAC GAC CTG	241
Asp Ile Ser Gly Lys Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu	
60 65 70 75	
ATC GCC CAG GGC AAC CTG AAC ACC GAG CTG AGC AAG GAG ATC CTT AAG	289
Ile Ala Gln Gly Asn Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys	
80 85 90	
ATC GCC AAC GAG CAG AAC CAG GTG CTG AAC GAC GTG AAC AAC AAG CTG	337
Ile Ala Asn Glu Gln Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu	
95 100 105	
GAC GCC ATC AAC ACC ATG CTG CGC GTG TAC CTG CCG AAG ATC ACC AGC	385
Asp Ala Ile Asn Thr Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser	
110 115 120	
ATG CTG AGC GAC GTG ATG AAG CAG AAC TAC GCC CTG AGC CTG CAG ATC	433
Met Leu Ser Asp Val Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile	
125 130 135	
GAG TAC CTG AGC AAG CAG CTG CAG GAG ATC AGC GAC AAG CTG GAC ATC	481
Glu Tyr Leu Ser Lys Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile	
140 145 150 155	
ATC AAC GTG AAC GTC CTG ATC AAC AGC ACC CTG ACC GAG ATC ACC CCG	529
Ile Asn Val Asn Val Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro	
160 165 170	
GCC TAC CAG CGC ATC AAG TAC GTG AAC GAG AAG TTC GAA GAG CTG ACC	577
Ala Tyr Gln Arg Ile Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr	
175 180 185	
TTC GCC ACC GAG ACC AGC AGC AAG GTG AAG AAG GAC GGC AGC CCG GCC	625
Phe Ala Thr Glu Thr Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala	
190 195 200	
GAC ATC CTG GAC GAG CTG ACC GAG CTG ACC GAG CTG GCC AAG AGC GTG	673

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Asp	Ile	Leu	Asp	Glu	Leu	Thr	Glu	Leu	Thr	Glu	Leu	Ala	Lys	Ser	Val		
205						210					215						
ACC	AAG	AAC	GAC	GTG	GAC	GGC	TTC	GAG	TTC	TAC	CTG	AAC	ACC	TTC	CAC	721	
Thr	Lys	Asn	Asp	Val	Asp	Gly	Phe	Glu	Phe	Tyr	Leu	Asn	Thr	Phe	His		
220					225					230					235		
GAC	GTG	ATG	GTG	GGC	AAC	AAC	CTG	TTC	GGC	CGC	AGC	GCC	CTG	AAG	ACC	769	
Asp	Val	Met	Val	Gly	Asn	Asn	Leu	Phe	Gly	Arg	Ser	Ala	Leu	Lys	Thr		
				240					245					250			
GCC	AGC	GAG	CTG	ATC	ACC	AAG	GAG	AAC	GTG	AAG	ACC	AGC	GGC	AGC	GAG	817	
Ala	Ser	Glu	Leu	Ile	Thr	Lys	Glu	Asn	Val	Lys	Thr	Ser	Gly	Ser	Glu		
			255					260					265				
GTG	GGC	AAC	GTG	TAC	AAC	TTC	CTG	ATC	GTG	CTG	ACC	GCC	CTG	CAG	GCC	865	
Val	Gly	Asn	Val	Tyr	Asn	Phe	Leu	Ile	Val	Leu	Thr	Ala	Leu	Gln	Ala		
		270					275					280					
CAG	GCC	TTC	CTG	ACC	CTG	ACC	ACC	TGT	CGC	AAG	CTG	CTG	GGC	CTG	GCC	913	
Gln	Ala	Phe	Leu	Thr	Leu	Thr	Thr	Cys	Arg	Lys	Leu	Leu	Gly	Leu	Ala		
	285					290					295						
GAC	ATC	GAC	TAC	ACC	AGC	ATC	ATG	AAC	GAG	CAC	TTG	AAC	AAG	GAG	AAG	961	
Asp	Ile	Asp	Tyr	Thr	Ser	Ile	Met	Asn	Glu	His	Leu	Asn	Lys	Glu	Lys		
300					305					310					315		
GAG	GAG	TTC	CGC	GTG	AAC	ATC	CTG	CCG	ACC	CTG	AGC	AAC	ACC	TTC	AGC	1009	
Glu	Glu	Phe	Arg	Val	Asn	Ile	Leu	Pro	Thr	Leu	Ser	Asn	Thr	Phe	Ser		
				320					325					330			
AAC	CCG	AAC	TAC	GCC	AAG	GTG	AAG	GGC	AGC	GAC	GAG	GAC	GCC	AAG	ATG	1057	
Asn	Pro	Asn	Tyr	Ala	Lys	Val	Lys	Gly	Ser	Asp	Glu	Asp	Ala	Lys	Met		
			335					340					345				
ATC	GTG	GAG	GCT	AAG	CCG	GGC	CAC	GGC	TTG	ATC	GGC	TTC	GAG	ATC	AGC	1105	
Ile	Val	Glu	Ala	Lys	Pro	Gly	His	Ala	Leu	Ile	Gly	Phe	Glu	Ile	Ser		
		350					355					360					
AAC	GAC	AGC	ATC	ACC	GTG	CTG	AAG	GTG	TAC	GAG	GCC	AAG	CTG	AAG	CAG	1153	
Asn	Asp	Ser	Ile	Thr	Val	Leu	Lys	Val	Tyr	Glu	Ala	Lys	Leu	Lys	Gln		
	365					370					375						
AAC	TAC	CAG	GTG	GAC	AAG	GAC	AGC	TTG	AGC	GAG	GTG	ATC	TAC	GGC	GAC	1201	
Asn	Tyr	Gln	Val	Asp	Lys	Asp	Ser	Leu	Ser	Glu	Val	Ile	Tyr	Gly	Asp		
380					385					390					395		
ATG	GAC	AAG	CTG	CTG	TGT	CCG	GAC	CAG	AGC	GAG	CAA	ATC	TAC	TAC	ACC	1249	
Met	Asp	Lys	Leu	Leu	Cys	Pro	Asp	Gln	Ser	Glu	Gln	Ile	Tyr	Tyr	Thr		
			400						405				410				
AAC	AAC	ATC	GTG	TTC	CCG	AAC	GAG	TAC	GTG	ATC	ACC	AAG	ATC	GAC	TTC	1297	
Asn	Asn	Ile	Val	Phe	Pro	Asn	Glu	Tyr	Val	Ile	Thr	Lys	Ile	Asp	Phe		
			415					420					425				

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ACC AAG AAG ATG AAG ACC CTG CGC TAC GAG GTG ACC GCC AAC TTC TAC Thr Lys Lys Met Lys Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr 430 435 440	1345
GAC AGC AGC ACC GGC GAG ATC GAC CTG AAC AAG AAG AAG GTG GAG AGC Asp Ser Ser Thr Gly Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser 445 450 455	1393
AGC GAG GCC GAG TAC CGC ACC CTG AGC GCG AAC GAC GAC GGC GTC TAC Ser Glu Ala Glu Tyr Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr 460 465 470 475	1441
ATG CCA CTG GGC GTG ATC AGC GAG ACC TTC CTG ACC CCG ATC AAC GGC Met Pro Leu Gly Val Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly 480 485 490	1489
TTT GGC CTG CAG GCC GAC GAG AAC AGC CGC CTG ATC ACC CTG ACC TGT Phe Gly Leu Gln Ala Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys 495 500 505	1537
AAG AGC TAC CTG CGC GAG CTG CTG CTA GCC ACC GAC CTG AGC AAC AAG Lys Ser Tyr Leu Arg Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys 510 515 520	1585
GAG ACC AAG CTG ATC GTG CCA CCG AGC GGC TTC ATC AGC AAC ATC GTG Glu Thr Lys Leu Ile Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val 525 530 535	1633
GAG AAC GGC AGC ATC GAG GAG GAC AAC CTG GAG CCG TGG AAG GCC AAC Glu Asn Gly Ser Ile Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn 540 545 550 555	1681
AAC AAG AAC GCC TAC GTG GAC CAC ACC GGC GGC GTG AAC GGC ACC AAG Asn Lys Asn Ala Tyr Val Asp His Thr Gly Gly Val Asn Gly Thr Lys 560 565 570	1729
GCC CTG TAC GTG CAC AAG GAC GGC GGC ATC AGC CAG TTC ATC GGC GAC Ala Leu Tyr Val His Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp 575 580 585	1777
AAG CTG AAG CCG AAG ACC GAG TAC GTG ATC CAG TAC ACC GTG AAG GGC Lys Leu Lys Pro Lys Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly 590 595 600	1825
AAG CCA TCG ATT CAC CTG AAG GAC GAG AAC ACC GGC TAC ATC CAC TAC Lys Pro Ser Ile His Leu Lys Asp Glu Asn Thr Gly Tyr Ile His Tyr 605 610 615	1873
GAG GAC ACC AAC AAC AAC CTG GAG GAC TAC CAG ACC ATC AAC AAG CGC Glu Asp Thr Asn Asn Asn Leu Glu Asp Tyr Gln Thr Ile Asn Lys Arg 620 625 630 635	1921
TTC ACC ACC GGC ACC GAC CTG AAG GGC GTG TAC CTG ATC CTG AAG AGC Phe Thr Thr Gly Thr Asp Leu Lys Gly Val Tyr Leu Ile Leu Lys Ser 640 645 650	1969

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CAG AAC GGC GAC GAG GCC TGG GGC GAC AAC TTC ATC ATC CTG GAG ATC Gln Asn Gly Asp Glu Ala Trp Gly Asp Asn Phe Ile Ile Leu Glu Ile 655 660 665	2017
AGC CCG AGC GAG AAG CTG CTG AGC CCG GAG CTG ATC AAC ACC AAC AAC Ser Pro Ser Glu Lys Leu Leu Ser Pro Glu Leu Ile Asn Thr Asn Asn 670 675 680	2065
TGG ACC AGC ACC GGC AGC ACC AAC ATC AGC GGC AAC ACC CTG ACC CTG Trp Thr Ser Thr Gly Ser Thr Asn Ile Ser Gly Asn Thr Leu Thr Leu 685 690 695	2113
TAC CAG GGC GGC CGG GGG ATT CTA AAA CAA AAC CTT CAA TTA GAT AGT Tyr Gln Gly Gly Arg Gly Ile Leu Lys Gln Asn Leu Gln Leu Asp Ser 700 705 710 715	2161
TTT TCA ACT TAT AGA GTG TAT TTT TCT GTG TCC GGA GAT GCT AAT GTA Phe Ser Thr Tyr Arg Val Tyr Phe Ser Val Ser Gly Asp Ala Asn Val 720 725 730	2209
AGG ATT AGA AAT TCT AGG GAA GTG TTA TTT GAA AAA AGA TAT ATG AGC Arg Ile Arg Asn Ser Arg Glu Val Leu Phe Glu Lys Arg Tyr Met Ser 735 740 745	2257
GGT GCT AAA GAT GTT TCT GAA ATG TTC ACT ACA AAA TTT GAG AAA GAT Gly Ala Lys Asp Val Ser Glu Met Phe Thr Thr Lys Phe Glu Lys Asp 750 755 760	2305
AAC TTT TAT ATA GAG CTT TCT CAA GGG AAT AAT TTA TAT GGT GGT CCT Asn Phe Tyr Ile Glu Leu Ser Gln Gly Asn Asn Leu Tyr Gly Gly Pro 765 770 775	2353
ATT GTA CAT TTT TAC GAT GTC TCT ATT AAG NAA GAT CGG GAT CTA ATA Ile Val His Phe Tyr Asp Val Ser Ile Lys Xaa Asp Arg Asp Leu Ile 780 785 790 795	2401
TTA ACA GTT TTT AAA AGC NAA TTC TTG TAT AAT GTC CTT GAT T Leu Thr Val Phe Lys Ser Xaa Phe Leu Tyr Asn Val Leu Asp 800 805	2444

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met	Asn	Lys	Asn	Asn	Thr	Lys	Leu	Ser	Thr	Arg	Ala	Leu	Pro	Ser	Phe
1				5					10					15	

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Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp
 20 25 30
 Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asp Leu Thr Leu
 35 40 45
 Asp Glu Ile Leu Lys Asn Gln Gln Leu Leu Asn Asp Ile Ser Gly Lys
 50 55 60
 Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn
 65 70 75 80
 Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln
 85 90 95
 Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Thr
 100 105 110
 Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val
 115 120 125
 Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys
 130 135 140
 Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val
 145 150 155 160
 Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile
 165 170 175
 Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr
 180 185 190
 Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Leu Asp Glu
 195 200 205
 Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val
 210 215 220
 Asp Gly Phe Glu Phe Tyr Leu Asn Thr Phe His Asp Val Met Val Gly
 225 230 235 240
 Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile
 245 250 255
 Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr
 260 265 270
 Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Gln Ala Phe Leu Thr
 275 280 285
 Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr
 290 295 300

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Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val
 305 310 315 320
 Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala
 325 330 335
 Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys
 340 345 350
 Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser Ile Thr
 355 360 365
 Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp
 370 375 380
 Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu
 385 390 395 400
 Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe
 405 410 415
 Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys
 420 425 430
 Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly
 435 440 445
 Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr
 450 455 460
 Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val
 465 470 475 480
 Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala
 485 490 495
 Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg
 500 505 510
 Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile
 515 520 525
 Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile
 530 535 540
 Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr
 545 550 555 560
 Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His
 565 570 575
 Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys
 580 585 590
 Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His

[illegible]

What is claimed is:

1. A substantially purified *Bacillus* strain which produces a pesticidal protein during vegetative growth wherein said *Bacillus* is not *B. sphaericus* SSII-1.
2. A *Bacillus* strain which produces a pesticidal protein during vegetative growth, wherein said *Bacillus* is *Bacillus cereus* having Accession No. NRRL B-21058.
3. A *Bacillus* strain which produces a pesticidal protein during vegetative growth, wherein said *Bacillus* is *Bacillus thuringiensis* having Accession No. NRRL B-21060
4. A *Bacillus* strain which produces a pesticidal protein during vegetative growth, wherein said *Bacillus* is a *Bacillus* selected from Accession Numbers NRRL B-21224, NRRL B-21225, NRRL B-21226, NRRL B-21227, NRRL B-21228, NRRL B-21229, NRRL B-21230, and NRRL B-21439.
5. An insect-specific protein isolatable during the vegetative growth phase of *Bacillus* spp. and components thereof, wherein said protein is not the mosquitocidal toxin from *B. sphaericus* SSII-1.
6. The insect-specific protein of claim 5 wherein said *Bacillus* is selected from a *Bacillus thuringiensis* and *B. cereus*.
7. The insect-specific protein of claim 5 wherein said protein is toxic to Coleoptera or Lepidoptera.
8. The insect-specific protein of claim 5 wherein the spectrum of insecticidal activity includes an activity against *Agrotis* and/or *Spodoptera* species, but preferably a black cutworm [*Agrotis ipsilon* ; BCW] and/or fall armyworm [*Spodoptera frugiperda*] and/or beet armyworm [*Spodoptera exigua*] and/or tobacco budworm and/or corn earworm [*Helicoverpa zea*] activity.
9. The insect-specific protein of claim 5, wherein said *Bacillus* is *Bacillus cereus* having Accession No. NRRL B-21058.
10. The insect-specific protein of claim 5, wherein said *Bacillus* is *Bacillus thuringiensis* having Accession No. NRRL B-21060.

11. The insect-specific protein of claim 5, wherein said *Bacillus* is a *Bacillus* selected from Accession Numbers NRRL B-21224, NRRL B-21225, NRRL B-21226, NRRL B-21227, NRRL B-21228, NRRL B-21229, NRRL B-21230, and NRRL B-21439.
12. The insect-specific protein of claim 5 wherein said protein has a molecular weight of about 30 kDa or greater.
13. The insect-specific protein of claim 12 wherein said protein has a molecular weight of about 60 to about 100 kDa.
14. The insect-specific protein of claim 13, wherein said protein has a molecular weight of about 80 kDa.
15. The insect-specific protein of claim 5, wherein said protein comprises a sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:5, SEQ ID NO:7, including homologues thereof.
16. The insect-specific protein of claim 5, wherein said protein has the sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:29 SEQ ID NO:32 and SEQ ID NO:2 including homologues thereof.
17. The insect-specific protein of claim 8, wherein said protein has the sequence selected from the group consisting of SEQ ID NO:29 and SEQ ID NO:32 including homologues thereof.
18. An insect-specific protein according to any one of claims 5 to 15, wherein the sequences representing the secretion signal have been removed or inactivated.
19. An auxiliary protein which enhances the insect-specific activity of an insect-specific protein.
20. The auxiliary protein of claim 19 wherein said auxiliary protein has a molecular weight of about 50 kDa.
21. The auxiliary protein of claim 19 wherein said auxiliary protein is from *Bacillus cereus*.
22. The auxiliary protein of any one of claims 19 to 21 wherein both the said auxiliary protein as well as said insect-specific protein is from strain AB78.

23. An auxiliary protein according to any one claims 19 to 22, wherein the sequences representing the secretion signal have been removed or inactivated.

24. A multimeric pesticidal protein, which comprises more than one polypeptide chain and wherein at least one of the said polypeptide chains represents an insect-specific protein of any one of claims 5 to 18 and at least one of the said polypeptide chains represents an auxiliary protein according to any one of claims 19 to 23, which activates or enhances the pesticidal activity of the said insect-specific protein.

25. The multimeric pesticidal protein according to claim 24 having a molecular weight of about 50 kDa to about 200 kDa.

26. The multimeric pesticidal protein of claim 25 comprising an insect-specific protein of any one of claims 5 to 18 and an auxiliary protein according to any one of claims 19 to 23, which activates or enhances the pesticidal activity of the said insect-specific protein.

27. A fusion protein comprising several protein domains including at least an insect-specific protein of any one of claims 5 to 18 and/or an auxiliary protein according to any one of claims 19 to 23 produced by in frame genetic fusions, which, when translated by ribosomes, produce a fusion protein with at least the combined attributes of the insect-specific protein of any one of claims 5 to 18 and/or an auxiliary protein according to any one of claims 19 to 23 and, optionally, of the other components used in the fusion.

28. A fusion protein according to claim 27, comprising a ribonuclease S-protein, an insect-specific protein of any one of claims 5 to 18 and an auxiliary protein according to any one of claims 19 to 23.

29. A fusion protein according to claim 27 comprising an insect-specific protein according to claim 5 and an auxiliary protein according to claim 19 having either the insect-specific protein or the auxiliary protein at the N-terminal end of the said fusion protein.

30. A fusion protein according to claim 29, comprising an insect-specific protein as given in SEQ ID NO:5 and an auxiliary protein as given in SEQ ID NO: 2 resulting in the protein given in SEQ ID NO: 23 including homologues thereof.

31. A fusion protein according to claim 29, comprising an insect-specific protein as given in SEQ ID NO:35 and an auxiliary protein as given in SEQ ID NO: 27 resulting in the protein given in SEQ ID NO: 50 including homologues thereof.
32. A fusion protein according to claim 28 comprising an insect-specific protein of any one of claims 5 to 18 and/or an auxiliary protein according to any one of claims 19 to 23 fused to a signal sequence, which is of heterologous origin with respect to the recipient protein.
33. A fusion protein according to claim 32, wherein the said signal sequence is a secretion signal.
34. A fusion protein according to claim 32, wherein the said signal sequence is a targeting sequence that directs the transgene product to a specific organelle or cell compartment.
35. A fusion protein according to claim 33 wherein the said protein has a sequence as given in SEQ ID NO: 43 including homologues thereof.
36. A fusion protein according to claim 34 wherein the said protein has a sequence as given in SEQ ID NO: 46 including homologues thereof.
37. A DNA molecule comprising a nucleotide sequence which encodes the protein of any one of claims 5-7, 9, 10, 12-15, and 19-22.
38. A DNA molecule comprising a nucleotide sequence which encodes the protein of any one of claims 8, 11, 16-18 and 23 to 36.
39. A DNA molecule comprising a nucleotide sequence which encodes an insect-specific protein isolatable during the vegetative growth phase of *Bacillus* spp. and components thereof, wherein said protein is not the mosquitocidal toxin from *B. sphaericus* SSII-1.
40. The DNA molecule of claim 39, wherein the said molecule comprises a nucleotide sequence as given in SEQ ID NO: 4, or SEQ ID NO: 6 including homologues thereof.
41. The DNA molecule of claim 39, wherein the said molecule comprises a nucleotide sequence as given SEQ ID NO:19, SEQ ID NO:28, SEQ ID NO:31, or SEQ ID NO:1 including homologues thereof.

42. A DNA molecule comprising a nucleotide sequence which encodes an auxiliary protein which enhances the insect-specific activity of an insect-specific protein.
43. The DNA molecule of claim 42 wherein the said molecule comprises a nucleotide sequence as given SEQ ID NO:19 including homologues thereof.
44. The DNA molecule according to any one of claims 37, 39, 40 or 42 which comprises a nucleotide sequence that has been optimized for expression in a microorganism.
45. The DNA molecule according to claim 37, 39, 40 or 42 which comprises a nucleotide sequence that has been optimized for expression in a plant.
46. The DNA molecule according to any one of claims 38, 41, or 43 which comprises a nucleotide sequence that has been wholly or partially optimized for expression in a microorganism.
47. The DNA molecule according to claim 38, 41 or 43 which comprises a nucleotide sequence that has been optimized for expression in a plant.
48. The DNA molecule of claim 45, wherein the said molecule comprises a nucleotide sequence as given in SEQ ID NO:17 or SEQ ID NO:18 including homologues thereof.
49. The DNA molecule of claim 47, wherein the said molecule comprises a nucleotide sequence as given in SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:27, or SEQ ID NO:30 including homologues thereof.
50. A DNA molecule which comprises a nucleotide sequence encoding a multimeric pesticidal protein, which comprises more than one polypeptide chains and wherein at least one of the said polypeptide chains represents an insect-specific protein of any one of claims 5 to 18 and at least one of the said polypeptide chains represents an auxiliary protein according to any one of claims 19 to 23, which activates or enhances the pesticidal activity of the said insect-specific protein.
51. The DNA molecule of claim 50 comprising a nucleotide sequence encoding an insect-specific protein of any one of claims 5 to 18 and an auxiliary protein according to any one of claims 19 to 23, which activates or enhances the pesticidal activity of the said insect-specific protein.

52. The DNA molecule of claim 51, wherein said molecule comprises a nucleotide sequence as given in SEQ ID NO:1 or SEQ ID NO:19 including homologues thereof.

53. A DNA molecule which encodes a fusion protein comprising several protein domains including at least an insect-specific protein of any one of claims 5 to 18 and/or an auxiliary protein according to any one of claims 19 to 23 produced by in frame genetic fusions, which, when translated by ribosomes, produce a fusion protein with at least the combined attributes of the insect-specific protein of any one of claims 5 to 18 and/or an auxiliary protein according to any one of claims 19 to 23 and, optionally, of the other components used in the fusion.

54. The DNA molecule of claim 53 which encodes a fusion protein comprising an insect-specific protein according to claim 5 and an auxiliary protein according to claim 19 having either the insect-specific protein or the auxiliary protein at the N-terminal end of the said fusion protein.

55. The DNA molecule of claim 53, wherein the said molecule comprises a nucleotide sequence as given in SEQ ID NO:22 including homologues thereof.

56. The DNA molecule of claim 53 which encodes a fusion protein comprising an insect-specific protein of any one of claims 5 to 18 and/or an auxiliary protein according to any one of claims 19 to 23 fused to a signal sequence, which is of heterologous origin respective to the recipient DNA.

57. The DNA molecule of claim 56, wherein the said signal sequence is a secretion signal.

58. The DNA molecule of claim 56, wherein the said signal sequence is a targeting sequence that directs the transgene product to a specific organelle or cell compartment.

59. The DNA molecule according to any one of claims 53 to 58, wherein at least one of its component sequences comprises a nucleotide sequence that has been optimized for expression in a microorganism.

60. The DNA molecule according to any one of claims 53 to 58, wherein at least one of its component sequences comprises a nucleotide sequence that has been optimized for expression in a plant.

61. The DNA molecule of claim 60, wherein the said molecule comprises a nucleotide sequence as given in SEQ ID NO:42, SEQ ID NO:45, or SEQ ID NO:49 including homologues thereof.
62. The DNA molecule of claim 45, wherein the sequences encoding the secretion signal have been removed from its 5' end.
63. The DNA molecule of claim 62, wherein the said molecule comprises a nucleotide sequence as given in SEQ ID NO: 35 or SEQ ID NO:39 including homologues thereof.
64. A DNA molecule which hybridizes to a DNA molecule according to any one of claims 37-63 under moderately stringent conditions and which molecule has insect-specific activity.
65. The DNA molecule of claim 64, wherein hybridization occurs at 65°C in a buffer comprising 7% SDS and 0.5 M sodium phosphate.
66. An insect specific protein wherein the said protein is encoded by a DNA molecule according to claims 64 or 65.
67. An expression cassette comprising a DNA molecule according to any one of claims 37, 39, 40, 42, 44, 45 or 48 operably linked to plant expression sequences including the transcriptional and translational regulatory signals necessary for expression of the associated DNA constructs in a host organism and optionally further regulatory sequences.
68. An expression cassette comprising a DNA molecule according to any one of claims 38, 41, 43, 46, 47 or 49-65 operably linked to plant expression sequences including the transcriptional and translational regulatory signals necessary for expression of the associated DNA constructs in a host organism and optionally further regulatory sequences.
69. An expression cassette according to claim 67, wherein the said host organism is a plant.
70. An expression cassette according to claim 68, wherein the said host organism is a plant.
71. A vector molecule comprising an expression cassette according to claim 67 or 69.
72. A vector molecule comprising an expression cassette according to claim 68 or 70.

73. An expression cassette according to claims 69 or 70 or a vector molecule according to claims 71 or 73 which is part of the plant genome.

74. A host organism comprising a DNA molecule according to any one of claims 37, 39, 40, 42, 44, 45 or 48, an expression cassette comprising the said DNA molecule or a vector molecule comprising the said expression cassette, preferably stably incorporated into the genome of the host organism..

75. A host organism comprising a DNA molecule according to any one of claims 38, 41, 43, 46, 47 or 49-65, an expression cassette comprising the said DNA molecule or a vector molecule comprising the said expression cassette, preferably stably incorporated into the genome of the host organism..

76. A host organism according to claim 74 or 75, selected from the group consisting of plant and insect cells, bacteria, yeast, baculoviruses, protozoa, nematodes and algae.

77. A transgenic plant including parts as well as progeny and seed thereof comprising a DNA molecule according to any one of claims 37, 39, 40, 42, 44, 45 or 48, an expression cassette comprising the said DNA molecule or a vector molecule comprising the said expression cassette, preferably stably incorporated into the plant genome.

78. A transgenic plant including parts as well as progeny and seed thereof comprising a DNA molecule according to any one of claims 38, 41, 43, 46, 47 or 49-65, an expression cassette comprising the said DNA molecule or a vector molecule comprising the said expression cassette, preferably stably incorporated into the plant genome.

79. A transgenic plant including parts as well as progeny and seed thereof which has been stably transformed with a DNA molecule according to any one of claims 38, 41, 43, 46, 47 or 49-65.

80. A transgenic plant including parts as well as progeny and seed thereof which expresses an insect-specific protein according to any one of claims 5, 7, 9, 10, 12-15, or 19-22.

81. A transgenic plant including parts as well as progeny and seed thereof which expresses an insect-specific protein according to any one of claims 8, 11, 16-18, 23-36 or 66.

82. The transgenic plant according to claim 80 or 81, which further expresses a second distinct insect control principle.
83. The transgenic plant of claim 82, wherein said second insect control principle is a *Bt* δ -endotoxin.
84. A transgenic plant according to any one of claims 77-83, which is a maize plant.
85. A transgenic plant according to any one of claims 77 to 84, which is a hybrid plant.
86. Plant propagating material of a plant according to any one of claims 77 to 84 treated with a seed protectant coating.
87. A microorganism transformed with an expression cassette according to any one of claims 67 to 70 and/or a vector molecule according to any one of claims 71 or 72, wherein the said microorganism is preferably a microorganism that multiply on plants.
88. The microorganism of claims 87, which is a root colonizing bacterium.
89. An encapsulated insect-specific protein which comprises a microorganism of any one of claims 87 or 88 comprising an insect specific protein according to claims 18 or 23.
90. An entomocidal composition comprising a host organism of any one of claims 74-76 in an insecticidally-effective amount together with a suitable carrier.
91. An entomocidal composition comprising a purified *Bacillus strain* according to any one of claims 1 to 4 in an insecticidally-effective amount together with a suitable carrier.
92. An entomocidal composition comprising an isolated protein molecule according to any one of claims 5 to 36 and 66, alone or in combination with a host organism of any one of claims 74-76 and/or an encapsulated insect-specific protein according to claim 89 in an insecticidally-effective amount, together with a suitable carrier.
93. A method of obtaining a purified insect-specific protein according to any one of claims 5 to 36 said method comprising applying a solution comprising said insect-specific protein to a NAD column and eluting bound protein.
94. A method for identifying insect activity of an insect-specific protein according to any one of claims 5 to 36, said method comprising:

- (a) growing a *Bacillus* strain in a culture;
- (b) obtaining supernatant from said culture;
- (c) allowing insect larvae to feed on diet with said supernatant; and,
- (d) determining mortality.

95. A method for isolating an insect-specific protein according to any one of claims 5 to 36, said method comprising:

- (a) growing a *Bacillus* strain in a culture;
- (b) obtaining supernatant from said culture; and,
- (c) isolating said insect-specific protein from said supernatant.

96. A method for isolating a DNA molecule comprising a nucleotide sequence encoding an insect-specific protein exhibiting the insecticidal activity of the proteins according to any one of claims 5 to 36, said method comprising:

- (a) obtaining a DNA molecule comprising a nucleotide sequence encoding an insect-specific protein; and
- (b) hybridizing said DNA molecule with DNA obtained from a *Bacillus* species; and
- (c) isolating said hybridized DNA.

97. A method of increasing insect target range by using an insect specific protein according to any one of claims 5 to 36 in combination with at least one second insecticidal protein that is different from the insect specific protein according to any one of claims 5 to 36.

98. A method of increasing insect target range wherein an insect specific protein according to any one of claims 5 to 36 is expressed in a plant together with a at least one second insecticidal protein that is different from the insect specific protein according to any one of claims 5 to 36.

99. A method according to claim 97 or 98 wherein the second insecticidal protein is selected from the group consisting of *Bt* δ -endotoxins, protease inhibitors, lectins, α -amylases and peroxidases.

100. A method of protecting plants against damage caused by an insect pest comprising applying to the plant or the growing area of the said plant an entomocidal composition according to any one of claims 90 to 92.

101. A method of protecting plants against damage caused by an insect pest comprising applying to the plant a toxin protein according to any one of claims 5 to 36.

102. A method of protecting plants against damage caused by an insect pest comprising planting a transgenic plant expressing a insect-specific protein according to any one of claims 5 to 36 within an area where the said insect pest may occur.

103. A method of producing a host organism according to claim 74 to 76 comprising transforming the said host organism with a DNA molecule according to any one of claims 67 to 70 and 73 or a vector molecule according to claim 71 and 72.

104. A method of producing a transgenic plant or plant cell according to any one of claims 77 to 85 comprising transforming the said plant and plant cell, respectively, with an expression cassette according to any one of claims 70 or 73 or a vector molecule according to claim 72.

105. A method of producing an entomocidal composition according to any one of claims 90 to 92 comprising mixing a *Bacillus* strain according to any one of claims 1 to 4 and/or a host organism according to claim 74 to 76 and/or an isolated protein molecule according to any one of claims 5 to 36 and 66, and/or an encapsulated protein according to claim 89 in an insecticidally-effective amount with a suitable carrier.

106. A method of producing transgenic progeny of a transgenic parent plant comprising stably incorporated into the plant genome a DNA molecule comprising a nucleotide sequence encoding an insect-specific protein according to any one of claims 5 to 36 and 66 comprising transforming the said parent plant with an expression cassette according to any one of claims 70 or 73 or a vector molecule according to claim 72, and transferring the pesticidal trait to the progeny of the said transgenic parent plant involving known plant breeding techniques.

107. A oligonucleotide probe capable of specifically hybridizing to a nucleotide sequence encoding an insect-specific protein isolatable during the vegetative growth phase of *Bacillus* spp. and components thereof, wherein said protein is not the mosquitocidal toxin from *B. sphaericus* SSII-1, wherein said probe comprises a contiguous portion of the coding sequence for the said insect-specific protein at least 10 nucleotides in length.

108. Use of a oligonucleotide probe for screening of any *Bacillus* strain or other organisms to determine whether the insect-specific protein is naturally present or whether a particular transformed organism includes the said gene.

109. A DNA molecule comprising a nucleotide sequence which encodes the protein of any one of claims 8, 11, 16-18 and 23 to 36 obtainable by a process comprising

(a) obtaining a DNA molecule comprising a nucleotide sequence encoding an insect-specific protein; and

(b) hybridizing said DNA molecule with an oligonucleotide probe according to claim 107 obtained from a DNA molecule comprising a nucleotide sequence as given in SEQ ID NO: 28, SEQ ID NO: 30, or SEQ ID NO: 31; and

(c) isolating said hybridized DNA.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 95/03826

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/32 C07K14/32 C07K14/325 C12N15/62 C12Q1/68
C12N15/82 A01N63/00 A01H5/00 C12N1/21 G01N33/00
//C07K16/12, C12N15/84, (C12N1/21, C12R1:07, 1:19, 1:085, 1:91)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K C12N A01N A01H C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	WO, A, 94 21795 (CIBA GEIGY AG ; WARREN GREGORY W (US); KOZIEL MICHAEL G (US); MULLI) 29 September 1994 see the whole document ---	1-109
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Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

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Date of the actual completion of the international search

16 January 1996

Date of mailing of the international search report

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Hix, R

INTERNATIONAL SEARCH REPORT

Int. onal Application No
PCT/EP 95/03826

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INTERNATIONAL SEARCH REPORT

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